

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 7, 2003, 11:19:49 ; Search time 38 Seconds

(without alignments)
1213.282 Million cell updates/sec

Title: US-09-909-775-2

Perfect score: 1879

Sequence: 1 MFLSILVALCLWLHLALGVR SPKKKNIKTRSAQKRTNPKRV 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:

908470

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

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6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

XX OS Homo sapiens .
XX PN WO200055629-A2.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1879	100.0	346	21 AA00193	Breast cancer prot
2	1879	100.0	346	22 AAB76853	Human lung tumour
3	1879	100.0	346	23 ABG61803	Prostate cancer as
4	1879	100.0	346	23 AAU85508	Clone #19118 of lu
5	1879	100.0	346	23 AA014432	Human frizzled rel
6	1870	99.5	368	19 AAW73508	Human ATG-1639 pro
7	1865	99.3	346	22 AAB48183	Human FRAZZLED pol
8	1865	99.3	368	20 AAY03232	Full length sequen
9	1862	99.1	368	20 AAW86346	Human FRAZZLED pro
10	1850	98.5	347	20 AAY03231	Amino acid sequenc

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

XX OS Homo sapiens .
XX PN WO200055629-A2.XX PD 21-SEP-2000 .
XX PF 15-MAR-2000; 2000WO-US06952.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

XX OS Homo sapiens .
XX PN WO200055629-A2.

XX PR 15-MAR-1999; 99US-0268865.

XX PR 12-NOV-1999; 99US-0439878.

XX PR 12-NOV-1999; 99US-0440370.

XX PR 15-NOV-1999; 99US-0440493.

XX PR 16-NOV-1999; 99US-0440676.

XX PR 16-NOV-1999; 99US-0440677.

XX PR 29-NOV-1999; 99US-0450810.

XX PR 02-DEC-1999; 99US-0453137.

XX PR 08-MAR-2000; 2000US-0453137.

PA	(EOSB-) EOS BIOTECHNOLOGY INC.	OS	Homo sapiens.
PI	MACK D, Gish KC;	XX	
XX	WP1; 2000-638216/61.	PN	WO200100828-A2.
DR	N-PSDB; AAA54127, AAA54128.	XX	
XX	Screening drug candidates for their ability to modulate breast cancer by contacting the drug to a cell expressing an expression profile gene and determining modulation of expression of the gene	PD	04-JAN-2001.
PT		XX	
XX		PF	30-JUN-2000; 2000WO-US18061.
PR		PR	30-JUN-1999; 99US-0346492.
XX		PR	15-OCT-1999; 99US-0419356.
PR		PR	17-DEC-1999; 99US-0466867.
PS		PR	30-DEC-1999; 99US-0476300.
XX		PR	06-MAR-2000; 2000US-0519642.
CC	New methods for screening drug candidates are described which comprise adding a drug candidate to a cell that expresses a protein selected from BC1H, BCA2, BCJ7, BCN1, BCN5, BCQ2, BCQ5, BCR2, BCX2 and BCY3 or their fragments and determining the effect of the drug on the expression of those proteins. Antibodies to breast cancer genes (specifically BC1H or its fragment (BC1H1 or BC1H2)) are useful for inhibiting and treating breast cancer in individuals who are non-responsive to anti-oestrogen and receptor. Compositions comprising BC1H or a nucleic acid encoding BC1H are useful for eliciting an immune response in an individual. The antibodies are also useful for the diagnosis and prognosis of breast cancer and for screening compositions which modulate the breast cancer phenotype. The method allows rapid and simple detection of lymph node metastases.	PR	22-MAR-2000; 2000US-0533077.
CC		PR	10-APR-2000; 2000US-0546259.
CC		PR	27-APR-2000; 2000US-0560406.
CC		PR	05-JUN-2000; 2000US-0589184.
PA	(CORTI-) CORIXA CORP.	PA	(CORTI-) CORIXA CORP.
PI	Wang T, Bangur CS, Iodes MJ,	PI	Wang T, Bangur CS, Iodes MJ,
PI	Retter MW, Mannion J;	PI	Retter MW, Mannion J;
XX		DR	WPI: 2001-071488/08.
XX	Lung tumor-associated proteins and the nucleic acids that encode them, useful for preventing, diagnosing and treating lung cancer -	XX	
PT		XX	
XX		XX	
PS	Example 1: Page 255-256; 436pp; English.	PS	Example 1: Page 255-256; 436pp; English.
XX		XX	
CC	The present invention describes immunogenic portions of lung tumour-associated proteins (1) and the nucleic acids (NAs) that encode them, CC have cytostatic activity and can be used in gene therapy, antisense CC inhibition and in vaccines. The NAs and the lung tumour-associated CC proteins may be used in the prevention, treatment and CC diagnosis of diseases associated with their inappropriate expression, CC especially lung cancers. For example, the NAs may be administered to CC treat diseases by rectifying mutations or deletions in a patient's genome CC or to supplement the patient's own production of (1). Additionally, the CC NAs may be used to produce the lung-tumour associated protein, according CC to standard recombinant DNA methodology. Conversely, antisense NA CC molecules may be administered to down regulate protein expression by CC binding with the cell's own genes and preventing their expression. The NA CC and complementary sequences may also be used as DNA probes in diagnostic CC assays to detect and quantify the presence of similar NA sequences in CC samples, and hence which patients may be in need of treatment for lung CC cancer. The (1) may be used as antigens in the production of antibodies CC and in assays to identify modulators (agonists and antagonists) of the CC expression and activity of the protein. AAF68083 to AAF68084 and CC AAB76848 to AAB76878 represent human lung tumour protein related CC nucleotide and protein sequences which are used in the exemplification CC of the present invention.	XX	
SQ	Sequence 346 AA;	SQ	Sequence 346 AA;
Query Match	Score 1879; DB 21; Length 346;	Query Match	Score 1879; DB 22; Length 346;
Best Local Similarity	100.0%; Pred. No. 4.6e-16;	Best Local Similarity	100.0%; Pred. No. 4.6e-176;
Matches	346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MFLSILVALCLMLHLALGVRAPEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAEIQ 60	Qy	1 MFLSILVALCLMLHLALGVRAPEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAEIQ 60
Db	1 MFLSILVALCLMLHLALGVRAPEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAEQ 60	Db	1 MFLSILVALCLMLHLALGVRAPEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAEQ 60
Qy	- 61 YEELVDVNCASVLRFFCAMAPICLDEFLPIKPKSYCORARDCEPLMKMYNHSWP 120	Qy	- 61 YEELVDVNCASVLRFFCAMAPICLDEFLPIKPKSYCORARDCEPLMKMYNHSWP 120
Db	61 YEELVDVNCASVLRFFCAMAPICLDEFLPIKPKSYCORARDCEPLMKMYNHSWP 120	Db	61 YEELVDVNCASVLRFFCAMAPICLDEFLPIKPKSYCORARDCEPLMKMYNHSWP 120
Qy	- 121 ESLACDELPVYDGVCTISPEALVTDLPEDVWIDTPDMMYQERPLDVCKRLSPDRCKC 180	Qy	- 121 ESLACDELPVYDGVCTISPEALVTDLPEDVWIDTPDMMYQERPLDVCKRLSPDRCKC 180
Db	121 ESLACDELPVYDGVCTISPEALVTDLPEDVWIDTPDMMYQERPLDVCKRLSPDRCKC 180	Db	121 ESLACDELPVYDGVCTISPEALVTDLPEDVWIDTPDMMYQERPLDVCKRLSPDRCKC 180
Qy	181 KKVKPTLATYLSKNYSVTHAKIVAYORSGCNEVTVDKEIKFSSSPIRTOVPLTN 240	Qy	181 KKVKPTLATYLSKNYSVTHAKIVAYORSGCNEVTVDKEIKFSSSPIRTOVPLTN 240
Db	181 KKVKPTLATYLSKNYSVTHAKIVAYORSGCNEVTVDKEIKFSSSPIRTOVPLTN 240	Db	181 KKVKPTLATYLSKNYSVTHAKIVAYORSGCNEVTVDKEIKFSSSPIRTOVPLTN 240
Qy	241 SSCQCQPHLPHODVLICYWESRMILLCLENVEKWRDQLSKRSIOWEERLQEQRRTVQD 300	Qy	241 SSCQCQPHLPHODVLICYWESRMILLCLENVEKWRDQLSKRSIOWEERLQEQRRTVQD 300
Db	241 SSCQCQPHLPHODVLICYWESRMILLCLENVEKWRDQLSKRSIOWEERLQEQRRTVQD 300	Db	241 SSCQCQPHLPHODVLICYWESRMILLCLENVEKWRDQLSKRSIOWEERLQEQRRTVQD 300
Qy	301 KKKTAGTTSRSNPPKPKGKPAPKPKASPKNKTRSAQKRINPKRV 346	Qy	301 KKKTAGTTSRSNPPKPKGKPAPKPKASPKNKTRSAQKRINPKRV 346
Db	301 KKKTAGTTSRSNPPKPKGKPAPKPKASPKNKTRSAQKRINPKRV 346	Db	301 KKKTAGTTSRSNPPKPKGKPAPKPKASPKNKTRSAQKRINPKRV 346
RESULT 2		Query Match	100.0%; Score 1879; DB 22; Length 346;
ID	AAB76853 standard; Protein: 346 AA.	Best Local Similarity	100.0%; Pred. No. 4.6e-176; Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		Qy	1 MFLSILVALCLMLHLALGVRAPEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAEIQ 60
AC	AAB76853;	Db	1 MFLSILVALCLMLHLALGVRAPEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAEIQ 60
XX		Qy	61 YEELVDVNCASVLRFFCAMAPICLDEFLPIKPKSYCORARDCEPLMKMYNHSWP 120
DT	12-APR-2001 (first entry)	Db	61 YEELVDVNCASVLRFFCAMAPICLDEFLPIKPKSYCORARDCEPLMKMYNHSWP 120
DE	Human lung tumour protein related protein sequence SEQ ID NO:329.	Qy	121 ESLACDELPVYDGVCTISPEALVTDLPEDVWIDTPDMMYQERPLDVCKRLSPDRCKC 180
XX		Db	121 ESLACDELPVYDGVCTISPEALVTDLPEDVWIDTPDMMYQERPLDVCKRLSPDRCKC 180
KW	Human; lung cancer; lung tumour protein; gene therapy;	Qy	181 KKVKPTLATYLSKNYSVTHAKIVAYORSGCNEVTVDKEIKFSSSP1PRTQVPLJTN 240
KW	lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;		
KW	cytostatic; antisense inhibition.		

				XX	Sequence	346 AA;
				Query Match	100.0%	Score 1879; DB 23; Length 346;
				Best Local Similarity	100.0%	Pred. No. 4.6e-176;
				Matches	346;	Conservative 0; Mismatches 0;
				Indels	0;	Gaps 0;
				QY	1	MFLSILVALCLWLHLALGYRGAPEAVRIPCMRIMPWNITRMPNHLHSTQENALIAEQ 60
				Db	1	MFLSILVALCLWLHLALGYRGAPEAVRIPCMRIMPWNITRMPNHLHSTQENALIAEQ 60
				QY	61	YEELVDVNGSAVLRFFFCAMYAPICITLEFLHDPIKPCSKVCQRADDCEPLMKMYNHSPW 120
				Db	61	YEELVDVNGSAVLRFFFCAMYAPICITLEFLHDPIKPCSKVCQRADDCEPLMKMYNHSPW 120
				QY	121	ESLADELPEVYDRCVICSEPAIVTDLPEVKWIDTPDMVQEPLDVCKRLSPDRCKC 180
				Db	121	ESLADELPEVYDRCVICSEPAIVTDLPEVKWIDTPDMVQEPLDVCKRLSPDRCKC 180
				QY	181	KKVKRPTLAYLSKNNSYVTHAKIKAVQRSQGCNEVTYVDKEIFKSSSPDPRQPLTN 240
				Db	181	KKVKRPTLAYLSKNNSYVTHAKIKAVQRSQGCNEVTYVDKEIFKSSSPDPRQPLTN 240
				QY	241	SSCOCPHILPHQDYLVIMCYEWRSRMMLLENCLVERWDOLSKRSIOWEEBLQEQRTVQD 300
				Qy	241	SSCOCPHILPHQDYLVIMCYEWRSRMMLLENCLVERWDOLSKRSIOWEEBLQEQRTVQD 300
				Db	241	SSCOCPHILPHQDYLVIMCYEWRSRMMLLENCLVERWDOLSKRSIOWEEBLQEQRTVQD 300
				QY	301	KKKTAGRTSRSNPPKPKGKPPAPKAPASPKNNIKTRSAQRTNPNRY 346
				Db	301	KKKTAGRTSRSNPPKPKGKPPAPKAPASPKNNIKTRSAQRTNPNRY 346
				RESULT 4		
				AAU85508		
				ID	AAU85508	standard; Protein: 346 AA.
				XX		
				AC	AAU85508;	
				XX		
				DT	21-MAY-2002	(first entry)
				XX		
				DE	#19118	of lung tumour protein.
				XX		
				XX		Lung tumour; cancer; T cell; immune response stimulator; cycostatic.
				XX		
				OS		Homo sapiens.
				XX		
				PN	WO200204514-A2.	
				XX		
				PD	17-JAN-2002.	
				XX		
				PF	10-JUL-2001;	2001WO-US22058.
				XX		
				PR	11-JUL-2000;	2000US-0614124.
				PR	29-AUG-2000;	2000US-0651563.
				PR	06-SEP-2000;	2000US-0658824.
				PR	26-SEP-2000;	2000US-0671325.
				PR	06-OCT-2000;	2000US-0677419.
				PR	30-OCT-2000;	2000US-0702705.
				PR	13-DEC-2000;	2000US-0736457.
				PR	03-MAY-2001;	2001US-0845626.
				PA	(CORI-X CORIXA CORP.	
				XX		
				PI	Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW,	
				PI	Marnerakis M, Carter D, Fanger GR, Vedick TS, Bangur CS;	
				PI	McNabb A, Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;	
				DR	WPI: 2002-164634/21.	
				DR	N-PSDB; ABK38056.	
				XX	Novel polynucleotide encoding a lung tumour polypeptide useful for	
				PT	stimulating and/or expanding T cells specific for a tumour protein	
				CC	ABG61800-ABG61944 represent prostate cancer-associated proteins.	

Example 1; SEQ ID No 329; 223pp; English.

The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for removing tumour cells from a biological sample. The polynucleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This is the amino acid sequence of a lung tumour associated protein, described in the method of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.

Q	A	Sequence	346	AA:
		Query Match	100.0%	Score 1879; DB 23; Length 346;
		Best Local Similarity	100.0%	pred. No. 4.6e-176;
		Matches	346;	Mismatches 0; Indels 0; gaps 0;
	a	MFLSILVALCLMHLAIGVRGACEAVRPICRHMPWNTTRMPNLIHLHSQEENALIAEQ	60	
	b	MFLSILVALCLMHLAIGVRGACEAVRPICRHMPWNTTRMPNLIHLHSQEENALIAEQ	60	
	y	YEELVDVNCASLVRFFCCAMAPICITLEFLDPPIKCKSQQRARDCEPLMKMYNHNSWP	120	
	b	YEELVDVNCASLVRFFCCAMAPICITLEFLDPPIKCKSQQRARDCEPLMKMYNHNSWP	120	
	y	ESLACDELPVYDGRGVCTSPSEAIVTDLPEVXWIDITPDMMMYQERPLDVCKRLSPDRCKC	180	
	b	ESLACDELPVYDGRGVCTSPSEAIVTDLPEVXWIDITPDMMMYQERPLDVCKRLSPDRCKC	180	
		KVKPFLATYLSKNSYVIHAKIKAVSGNEVTTVVDKEIFSSSPPTROVLITN	240	
		KVKPFLATYLSKNSYVIHAKIKAVSGNEVTTVVDKEIFSSSPPTROVLITN	240	

RESULT 5	
A014432	AA014432 standard; Protein; 346 AA.
D	
X	
C	AA014432;
X	
T	03-MAY-2002 (first entry)
X	
E	Human frizzled related protein 4 (FRP-4).
X	
H	Human; phosphate homeostasis modulation; frizzled related protein-4;
W	FRP-4; phosphate transportation; serum phosphate concentration;
W	hypophosphataemia; phosphaturia; 1,25-dihydroxy vitamin D deficiency;
W	osteomalacia; phosphate homeostasis related disease;
W	X-linked hypophosphataemia; rickets; oncogenic osteomalacia;
W	rhabdomyopathy; tumoral calcinosis; renal failure;
W	bone mineralisation.
X	
S	Homo sapiens.
X	

X WO200205857-A2.
X
X 24-JAN-2002.
C
X 19-JUL-2001: 2001WO-US233014
F

XX
 PR 19-JUL-2000; 20000US-219365P.
 PR 12-JAN-2001; 2001US-261438P.
 XX
 PA (GENZ) GENZYME CORP.
 XX
 PI Schiavi S, Madden SL,
 XX Manavalan P, Levine M, De Beur SJ;
 XX
 DR WPL; 2002-179752/23.
 DR N-PSDB; AAL41901.
 XX
 PT Modulating phosphate homeostasis in a subject, for alleviating the
 oncogenic osteomalacia associated symptoms, comprises altering the
 activity of frizzled related protein-4 (FRP4) or a gene encoding FRP-4
 polypeptide

xx Disclosure; Fig 2; 51pp; English.
xx PS
xx CC The invention comprises a method for modulating phosphate homeostasis in
xx CC a subject. The method involves altering the activity of the frizzled
xx CC related protein-4 (FRP-4), or altering the expression of the FRP-4 gene.
xx CC Phosphate plays a critical role in many cellular processes essential to
xx CC normal functionality of the human body. Phosphate homeostasis is
xx CC primarily regulated by the kidney, largely through variation in renal
xx CC tubular re-absorption of phosphate. Alterations of the phosphate
xx CC transporting function of the kidney and subsequent disturbance of serum
xx CC phosphate concentration often lead to serious biochemical and clinical
xx CC problems. The method of the invention is useful for modulating phosphate
xx CC homeostasis in a subject. The method of the invention can be used to
xx CC alleviate oncogenic osteomalacia associated symptoms (e.g.,
xx CC hypophosphataemia, phosphaturia, low serum concentrations of 1,25-
xx CC dihydroxy vitamin D and osteomalacia). The method of the invention can
xx CC also be used to treat phosphate homeostasis related diseases (e.g.,
xx CC rhabdomyolysis, rickets, oncogenic osteomalacia,
xx CC cardiomopathy, tumoral calcinosis, renal failure and
xx CC bone mineralisation). The present amino acid sequence represents the
xx CC human frizzled related protein 4 (FRP-4).
xx Sequence 346 AA:
xx SQ

Query	Match	Start	End	Score	Length	DB
Qy	1	MFLSILVALCWLHIALGVAGPCEAVRIMCRAMPWNTRMPNHLHSTQENAIIATEQ	60	100	0%	Score 1879; DB 23; Length 346;
Best Local Matches	1	MFLSILVALCWLHIALGVAGPCEAVRIMCRAMPWNTRMPNHLHSTQENAIIATEQ	60	100	0%	Pred. No. 4.6e-176; Mismatches 0; Gaps 0;
Db	1	YEELDVNCASVLRFEEFCAMAYAPICTLEFLHDPIKPCSKYCQRARDCEPLMKMYNHNSWP	120	61	YEELDVNCASVLRFEEFCAMAYAPICTLEFLHDPIKPCSKYCQRARDCEPLMKMYNHNSWP	120
Qy	61	ESLACDELDPYDRGVCISPSAIAVTLDPEDYKWDITPDNMWQERPLDVKRLSPDRCKC	180	61	ESLACDELDPYDRGVCISPSAIAVTLDPEDYKWDITPDNMWQERPLDVKRLSPDRCKC	180
Db	61	KVKPILATYLSKNSYVIHAKIRAVQRSGGNEVPTVDYKEIFKSSSP; PRTQVPLITN	240	121	KVKPILATYLSKNSYVIHAKIRAVQRSGGNEVPTVDYKEIFKSSSP; PRTQVPLITN	240
Qy	121	SSQCQPHILPHQDVLMCYEWRSRMMLLENCLYEVKWRDQLSKRSIOWEERLQEQRRTYQD	300	181	SSQCQPHILPHQDVLMCYEWRSRMMLLENCLYEVKWRDQLSKRSIOWEERLQEQRRTYQD	300
Db	121	KKKTAGRTSSSNPPPKCKPAPKAPSKPNKIKPSAQKETNPKRV	346	241	KKKTAGRTSSSNPPPKCKPAPKAPSKPNKIKPSAQKETNPKRV	346
Qy	241	KKKTAGRTSSSNPPPKCKPAPKAPSKPNKIKPSAQKETNPKRV	346	301	KKKTAGRTSSSNPPPKCKPAPKAPSKPNKIKPSAQKETNPKRV	346
Db	241	KKKTAGRTSSSNPPPKCKPAPKAPSKPNKIKPSAQKETNPKRV	346	301	KKKTAGRTSSSNPPPKCKPAPKAPSKPNKIKPSAQKETNPKRV	346

RESULT 6 ✓
AAW73508 ID AAW73508 standard; Protein; 368 AA.
XX

Db 125 ACDELPLYDRGVCISPEAVITDLPEDVKWIDITPDMMVQERPLDVGCKRLSPDRCKKKV 184
 QY 184 KPTLATTLSKNSYYIAKIKAVQRSGCNEVTTVDKEIFKSSSP:PTRVQLPTLNSSC 243
 Db 185 KPTLATTLSKNSYYIAKIKAVQRSGCNEVTTVDKEIFKSSSP:PTRVQLPTLNSSC 244
 QY 244 QCPHILPHDILMCYEMRSRMLLENCLVEKWDQLSKRSQWEERLQEQRRTVQDKKK 303
 Db 245 QCPHILPHDILMCYEMRSRMLLENCLVEKWDQLSKRSQWEERLQEQRRTVQDKKK 304
 QY 304 TAGTRSRNPKPKGKPPAKPASKPKNNIKTSQAQRTNPKV 346
 Db 305 TAGTRSRNPKPKGKTPAKPKASKPKNNIKTSQAQRTNPKV 347

RESULT 11
 ID AAB23911 standard; Protein: 346 AA.
 XX
 AC AAB23911;
 XX DT 17-JAN-2001 (first entry)
 DE Bos taurus Frazzled protein SEQ ID NO:2.
 XX
 Bovine; Bos taurus; frazzled protein; FRZB family; cytostatic; antiHIV;
 KW human immunodeficiency virus; nootropic; neuroprotective;
 KW antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW cerebroprotective; antiarteriosclerotic; osteopathic; ophthalmological;
 KW antisporadic; cartilage; bone morphogenesis; regulator; inflammation;
 KW arthritis; rheumatoid arthritis; osteoarthritis; septicemia; stroke;
 KW autoimmune disease; transplant rejection; graft versus host disease;
 KW infection; ischaemia; renal disorder; restenosis; brain injury; AIDS;
 KW bone disease; osteoporosis; cancer; lymphoproliferative disorder;
 KW atherosclerosis; Alzheimer's disease; retinitis pigmentosa;
 KW macular degeneration; degenerative eye disease.
 OS Bos taurus.
 XX PN WO200055202-A1.
 XX PD 21-SEP-2000.
 XX PF 15-MAR-2000; 2000WO-US06820.
 XX PR 18-MAR-1999; 99US-0125038.
 PR 03-MAR-2000; 2000US-0519397.
 XX PA {SMIK } SMITHKLINE BEECHAM CORP.
 PA {SMIK } SMITHKLINE BEECHAM PLC.
 XX PI James IE, Lark MW, Testa TT;
 XX WPI; 2000-633181/61.
 DR N-PSDB; AAA93046.
 XX PS Claim 2; Page 27; 29pp; English.

bowel disease, psoriasis), transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, renal disorder, restenosis, brain injury, AIDS, metabolic and other bone diseases (e.g. osteoporosis), cancer (e.g. lymphoproliferative disorders), atherosclerosis, Alzheimer's disease, retinitis pigmentosa, macular degeneration and other degenerative eye diseases. The protein is also useful to establish assays to predict oral absorption and pharmacokinetics in man and thus enhance compound and formulation design, and in screening assays. The polynucleotide is useful for recombinant production of the frazzled protein.

Sequence 346 AA:

Query	Match	Score 1807;	DB 21;	Length 346;
Best	Local Similarity	96.2%;	Prod. No. 5.5e-169;	
Matches	Conservative	95.9%;	Mismatches 9;	Indels 0;
Db	1 MFLSILVALCLWLALGVRGAPECAVRIPMGRHMPNITRMPNLHSTQENAILAEQ 60			
QY	1 MFLSILVALCLWLALGVRGAPECAVRIPMGRHMPNITRMPNLHSTQENAILAEQ 60			
Db	1 MLLSLTALCLWLALGVRGAPECAVRIPMGRHMPNITRMPNLHSTQENAILAEQ 60			
QY	61 YEEFLVDVNCASAVLRFIFCFAMYAPICTEFLIDPIPKPSVCAORDECEPLMKMYNISWP 120			
Db	61 YEEFLVDVNCASAVLRFIFCFAMYAPICTEFLIDPIPKPSVCAORDECEPLMKMYNISWP 120			
QY	121 ESLACDELPLYDRGVCISPEAVITDLPEDVKWIDITPDMMVQERPLDVGCKRLSPDRCKC 180			
Db	121 ESLACDELPLYDRGVCISPEAVITDLPEDVKWIDITPDMMVQERPLDVGCKRLSPDRCKC 180			
QY	181 KKVKPPTLATYLSKNSYTHAIKIKAVQRSGCNEVTTVDKEIFKSSSP1PTQVPLITN 240			
Db	181 KKVKPPTLATYLSKNSYTHAIKIKAVQRSGCNEVTTVDKEIFKSSSP1PTQVPLITN 240			
QY	241 SSCQCPhIPHDYLTCYEWSSRMMLLENCIVEKWDQLSKRSRSSIONEERIQEQRRTVQD 300			
Db	241 SSCQCPhIPHDYLTCYEWSSRMMLLENCIVEKWDQLSKRSRSSIONEERIQEQRRTVQD 300			
QY	301 KKKTAGRTSRNSNPKPCKPARKPASKPKNNIKTSAQRTNPKR 345			
Db	301 KKRTAGRTSRNSNAPKPKGKPPAKPKASKPKNNIKTSAQRTNPKR 345			

RESULT 12

AAW86347	AAW86347 standard; Protein: 372 AA.
1D	AAW86347;
XX	AAW86347;
AC	AAW86347;
XX	AAW86347;
DT	15-MAR-1999 (first entry)
XX	Partial human FRAZZLED protein.
DE	
XX	
KW	Human; FRAZZLED protein; FRZB; chronic inflammation; acute inflammation; arthritis; osteoarthritis; septicemia; autoimmune disease; cancer; transplant rejection; graft versus host disease; infection; stroke; ischaemia; acute respiratory disease syndrome; renal disorder; restenosis; brain injury; AIDS; cancer.
XX	
OS	Homo sapiens.
XX	
FH	Key Misc-difference 19
FT	Location/Qualifiers /label= unknown /note= "encoded by GAN"

The present sequence represents bovine (Bos taurus) Frazzled protein which is a member of the FRZB family. The frazzled protein can have cytostatic, antiHIV (human immunodeficiency virus), nootropic, vasoconstrictive, neuroprotective, antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, cerebroprotective, osteopathic, antiarteriosclerotic, ophthalmological and antisporadic activities, and is a regulator of cartilage and bone morphogenesis. The frazzled polynucleotide and protein are useful for treating and preventing chronic and acute inflammation, arthritis, rheumatoid arthritis, osteoarthritis, septicemia, autoimmune diseases (e.g. inflammatory

XX	PA	(SMIK) SMITHKLINE BEECHAM CORP.	XX	XX	02-APR-2001 (first entry)	
XX	PI	James I, Kumar S, Lark M;	XX	DE	Partial amino acid sequence of human FRAZLED polypeptide.	
XX	DR	WPI: 1999-047873/05.	XX	KW	FRAZLED; antiinflammatory; osteopathic; immunosuppressive; AIDS;	
XX	N-PSDB;	AAV80658.	XX	KW	antiarthritic; cerebroprotective; vasoactive; nephrotropic; antiHIV;	
PT	New FRAZB -related (FRAZLED) polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of cancer, Alzheimer's disease and AIDS	XX	KW	cystostatic; antiarteriosclerotic; nootropic; neuroprotective; vaccine; gene therapy; human.		
XX	PT		XX	KW	Homo sapiens.	
PS	Example 1: Page 11: 25pp: English.	XX	Key	Misc-difference 19	Location/Qualifiers	
XX	CC	The present sequence represents partial human FRAZLED protein from the FRAZB family. The FRAZB family controls signalling and developmental patterning. FRAZLED proteins and polynucleotides are useful for diagnosing diseases related to over or underexpression of FRAZLED protein by identifying mutations in the FRAZLED gene, or determining FRAZLED protein expression levels. FRAZLED proteins can be used to screen for agonists and antagonists which bind the FRAZLED protein by observing the binding, or stimulation or inhibition of FRAZLED activity. These can be used in treatment to activate (agonist) or inhibit (antagonist) FRAZLED activity, in addition to direct administration of antisense sequences to prevent expression, or FRAZLED polynucleotides to treat conditions associated with lack of FRAZLED protein. Gene therapy may also be used to affect endogenous FRAZLED protein production. FRAZLED antibodies are useful for inducing an immune response to immune and prevent diseases, and for isolating FRAZLED clones or purify the protein by affinity chromatography.	FT	/label= unknown /note= "encoded by GAN"		
CC	CC	Inhibit (antagonist) FRAZLED activity, in addition to direct administration of antisense sequences to prevent expression, or FRAZLED polynucleotides to treat conditions associated with chronic and acute inflammation, diagnosis, arthritis, osteoarthritis, septicemia, autoimmune diseases, transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, renal disorders, restenosis, brain injury, AIDS and cancer.	FT	XX		
XX	SQ	Sequence 372 AA:	FT	XX		
CC	Query Match 93.9%; Score 1765; DB 20; Length 372; Best Local Similarity 94.6%; Pred. No. 8.1e-165; Matches 331; Conservative 2; Mismatches 13; Indels 4; Gaps 2;	CC	CC	CC	CC	
QY	1 MFLSILVALCLWHLAQLGVRGAP-CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAE 59	Db	23 MFLSILVALCLWHLAQLGVRGAP-CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAE 82	CC	CC	
QY	60 QYEELVDVNCSAVLRFECAMKAPICITLELHDPIPKCKSVQRADDCEPLIMKMYNHSW 119	Db	83 QYEELVDVNCSAVLRFECAMKAPICITLELHDPIPKCKSVQRADDCEPLIMKMYNHSW 142	CC	CC	
QY	120 PESLACDLPYDGVCTSPSEAIVTDLPEVDKWLIDTPDMMAQERPDVKWLSDPRCK 179	Db	143 PESLACDLPYDGVCTSPSEAIVTDLPEVDKWLIDTPDMMAQERPDVKWLSDPRCK 202	CC	CC	
QY	180 CKVKPPTLATYLSKNSYVTHAKIKAVQRSGNEVTVVYDKEIFKSSSPIPRTQVLIT 239	Db	203 CKVKPPTLATYLSKNSYVTHAKIKAVQRSGNEVTVVYDKEIFKSSSPIPRTQVLIT 262	CC	CC	
QY	240 NSSCQCPHILPQDVLIMCYEARSRMMLENCLVEKWDLSKRSIOWERLQEQRRTVQ 299	Db	263 NSSCQCPHILPQDVLIMCYEARSRMMLENCLVEKWDLSKRSIOWERLQEQRRTVQ 322	CC	CC	
QY	300 DKKTAGRTSRSNPKPKGKPPAKPKSPKNNIKTR--SAOKRTNPKRV 346	Db	323 DKKTAGRTSRSNPKPKGKTPAKPKSPKNNIKTRGPRTKRNPKRV 372	CC	CC	
QY	344 1 MFLSILVALCLWHLAQLGVRGAP-CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAE 59	Db	367 23 MFLSILVALCLWHLAQLGVRGAP-CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAE 82	CC	CC	
QY	60 QYEELVDVNCSAVLRFECAMKAPICITLELHDPIPKCKSVQRADDCEPLIMKMYNHSW 119	Db	83 QYEELVDVNCSAVLRFECAMKAPICITLELHDPIPKCKSVQRADDCEPLIMKMYNHSW 142	CC	CC	
RESULT 13						
AAB48184	ID AAB48184 standard; Protein; 372 AA.					
XX						
AC						

Qy	120 PESIACDELPPYDRCYCISPEIAIVTDLPEDVKWIDITPDMMVQERPLDVCKRLSPDRCK	179	Qy	123 IACDELPYDRCYCISPEIAIVTDLPEDVKWIDITPDMMVQERPLDVCKRLSPDRCK	178
Db	143 PESIACDELPPYDRCYCISPEIAIVTDLPEDVKWIDITPDMMVQERPLDVCKRLSPDRCK	202	Db	134 LACEELPYDRCYCISPEIAIVTDLPEDVKWIDITPDMMVQERPLDVCKRLSPDRCK	178
Qy	180 CKKVKPTLATTLSKNSYVHAKIKAVQRSGNEVITYVDKEIFKSSPPIRTOVLIT	239	Qy	179 KCKKVKTPLATTLSKNSYVHAKIKAVQRSGNEVITYVDKEIFKSSPPIRTOVLIT	237
Db	203 CKKVKPTLATTLSKNSYVHAKIKAVQRSGNEVITYVDKEIFKSSPPIRTOVLIT	262	Db	179 KCKPVTKTQKTYFRNNNYVIRAKVEI-KTKCHDVAVVEKEILSSLVNPYDVTNL	237
Qy	240 NSSCQCOPHILPHODVLIMCYEVRSRMILLENCLVEKWRDOLSKRSIOWEEERLQEORTVQ	299	Qy	238 ITNSSCCPHILPHODVLIMCYEVRSRMILLENCLVEKWRDOLSKRSIOWEEERLQEORTVQ	295
Db	263 NSSCQCOPHILPHODVLIMCYEVRSRMILLENCLVEKWRDQLSKRSIOWEEERLQEQRRTVQ	322	Db	238 YTSGCLCPPLNVNEEVYLIGYEDEEESRLLVVEGSIAEKAKDRUGKVKRWDMLKLHLG	297
Qy	300 DKKTAGRTSRSNPPPKGKPKPAKPASKPKNIKTR--SAQKRTNPKRV	346	Qy	296 RTVQDKKKTAGRTS--SNP	313
Db	323 DKKTAGRTSRSNPPPKGKPKGTAPKPKPAKPASKPKNIKTRGRPTPKRTNPKRV	372	Db	298 LSKSDSSNSDSTSQSKSGRNNSNP	320
<hr/>					
RESULT 14					
AAW41767	AAW41767 standard; Protein: 325 AA.		AAW41767	AAW41767 standard; Protein: 325 AA.	
XX			XX	AAW41767;	
AC			AC	AAW41767;	
XX			XX	AAW41767;	
DT	28-SEP-1998 (first entry)		DT	04-SEP-1998 (first entry)	
XX			XX	04-SEP-1998 (first entry)	
DE	Human hsfz protein.		DE	Bovine growth-inducing protein Frzb sequence.	
XX			XX	Frzb: growth-inducing protein; bovine; human; Xenopus; cartilage;	
KW	Human; nerve cell growth factor; hsfz protein; neuronal cell;		KW	KW bone; nerve; muscle; tumour; Wnt-expressing tumour; myodegeneration;	
KW	proliferation; differentiation factor.		KW	KW subglottic stenosis; chondromalacia patellae; osteoarthritis;	
XX			KW	KW joint surface lesion; neurodegeneration; Alzheimer's disease;	
OS	Homo sapiens.		KW	KW osteodegeneration; angiogenesis; wound healing.	
XX			XX	Bos sp.	
PN	DE19702835-A1.		OS	XX	
XX			XX	Key	Location/Qualifiers
PD	22-JAN-1998.		PF	FH	
XX			PF	Peptide	
PF	.27-JAN-1997; 97DE-1002835.		FT	FT	
XX			FT	Cleavage-site	
PR	09-JUL-1996; 96DE-1027631.		FT	FT	
XX			FT	FT	
PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.		FT	FT	
XX			FT	FT	
PI	Deutsch U, Drexler JCA, Lottspeich F, Mayr T, Risau W;		FT	FT	
PI	Rohrer H;		FT	FT	
XX			FT	FT	
DR	WP: 1998-088096/09.		FT	FT	
DR	N-PSDB; AAV13101.		FT	FT	
XX			FT	FT	
PN	W09816641-A1.		XX	XX	
PT	New nucleic acid encoding protein that increases neuronal cell		PN	W09816641-A1.	
PT	proliferation - useful as nerve growth factor and for detection or		XX	XX	
PT	inhibition of differentiation factors		PD	23-APR-1998.	
XX			PD	23-APR-1998.	
PS	Claim 5; Page 17; 27pp; German.		PF	08-OCT-1997;	
XX			PF	08-OCT-1997;	
CC	This sequence represents the human hsfz protein. This protein is found to		XX	97WO-US18362.	
CC	increase the proliferation of neuronal cells. Such proteins can be used		PR	20-MAR-1997;	
CC	as nerve cell growth factors and for the detection and/or inhibition of		PR	97US-0022333.	
CC	differentiation factors, specifically those corresponding to the		XX	11-OCT-1996;	
CC	Drosophila melanogaster wingless or mouse int-1 type.		XX	96US-0729452.	
XX			PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
SQ	Sequence 325 AA;		PI	Hoang B, Luyten FP, Moos M, Wang S;	
XX			XX	XX	
Query Match	44.2%; Score 831; DB 19; Length 325;		DR	WPI: 1998-251288/22.	
Best Local Similarity	50.8%; Pred. No. 4.3e-73;		DR	N-PSDB; AAV13101.	
Matches	164; Conservative 52; Mismatches 77; Indels 30; Gaps 8;		XX	XX	
CC	This sequence represents the human hsfz protein. This protein is found to		PT	New nucleic acid encoding human, bovine and Xenopus Frzb protein -	
CC	increase the proliferation of neuronal cells. Such proteins can be used		PT	PT and related proteins, antibodies, peptides), vectors and	
CC	as nerve cell growth factors and for the detection and/or inhibition of		PT	PT transformed cells, used to induce growth of cartilage, bone, nerve	
CC	differentiation factors, specifically those corresponding to the		PT	PT and muscle, also for inhibiting Wnt-expressing tumours	
XX	Drosophila melanogaster wingless or mouse int-1 type.		XX	XX	
PS	Query 1; Fig 1; 66pp; English.		PS	Claim 4; Fig 1; 66pp; English.	
XX			XX	This represents a bovine growth-inducting protein Frzb. Bovine, human	
CC			CC	and Xenopus Frzb genes which are shown in AAV18253 to AAV18255 are	
CC			CC		

related to the frizzled gene in Drosophila. The corresponding bovine, human and Xenopus Frzb protein sequences are shown in AAW48664 to AAW48696. A recombinant construct containing a Frzb encoding nucleic acid linked to a heterologous promoter in an expression vector can be used to produce recombinant Frzb proteins. The Frzb proteins may be formulated with fibrin glue, freeze-dried cartilage grafts or collagen (optionally also cartilage progenitor cells, chondroblasts or chondrocytes). They are coated on to, or mixed with, a (non-)resorbable matrix, or mixed with a biodegradable polymer. They modulate activity of the growth factors Wnt-1 to 8. The Frzb proteins induce skeletal morphogenesis, embryonic pattern formation and tissue specificity and are used to induce growth of cartilage, bone, nerve and muscle, particularly in cases of subglottic stenosis, chondromalacia patellae, osteoarthritis, joint surface lesions, neurodegeneration (e.g. Alzheimer's disease), myodegeneration or osteodegeneration. They also modulate Wnt-mediated signalling in cells, and are used to inhibit growth of Wnt-expressing tumours (particularly mammary or intestinal). The Frzb genes may also be used to identify specific modulators or as a growth factor for cells of the chondrocyte lineage in vitro, to stimulate wound healing, to promote angiogenesis, to prevent transplant rejection and as adjunct to chemotherapy or immunotherapy. Fragments of Frzb proteins are used for detecting genetic abnormalities associated with Frzb genes.

Seq	Sequence	325 AA:	Query Match	Score	DB	Length
			Best Local Similarity	44.2%	Score 831; DB 19;	Length 325;
			Matches 166; Conservative	51.4% ; Pred. No. 4.3e-73;	No. 4.3e-73;	
			Db	16	Indels 32; Gaps 8;	
Qy	LSILVALCLWLHLALGYRGAPCEAVRIPCMCRHMWNITRMPNHLHISTQANIALEEQYE	62	3			
Db	LLALAALCL-LRVP-GARAACEPVPRILCKSLPWNMTKWNHLHISTQANIALEEQFE	73				
Qy	ELVDVNSCAVLFVFFCAMYAPICLTLFLHDPIKPCSVCORARDCEPLKMYNNISWPES	122	63			
Db	GLGTHGSPDLFLFCAMYAPICLTDQHEP IKPCSVCORARQGPBPILKRYHHSWPES	133	74			
Qy	LACDELPPYDRCYCISPEAIVT---DLPEDYKWIDTPDMVQERPLDVDCKRSLSPDRC	178	123			
Db	LACEELPPYDRCYCISPEAIVTADGADFPMDS-----	178	134			
Qy	KCKKVPRPLATYLSKNSVYIHKAKIVQRSGCNEVTVDYKEIPEKSS-SPIPRHQVPL	237	179			
Db	KCKPVPRATQKYFRNNNNYVIRAKVEI-KTKCHDVTAVVEKEILKASLYNPRETVNVL	237	179			
Qy	ITNSSCOPPHILPHQDYLMCY- -EVRSRMILLLENCLVEKWRDOLSKRSOWERLQEQR	295	238			
Db	YTSSGGCLCPPLRVNEEYLIMGYDEERSRLLVEGSTAEKWMDRLLRKVKRWDMKLRLHG	297	238			
Qy	RIVQD-----KKTAGRTSRS 311		296			
Db	LNTSDSSHSDSTQSQRPGRNSNS 320		298			

Search completed: March 7, 2003, 11:23:56
Job time : 40 secs

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Query Match 44 1%; Score 828; DB 4; Length 325;
 Best Local Similarity 50.8%; Pred. No. 3.3e-74; DB 4; Length 318;
 Matches 164; Conservative 51; Mismatches 78; Indels 34; Gaps 8;

Query 3 LSILVALCMLHLLAUGVRGAPCEAVRPMNITRPNLHLHSTQANALIAEQY 62

RESULT 2
 US-08-878-474-9
 Sequence 9, Application US/08878474
 Patent No. 6133232

GENERAL INFORMATION:
 APPLICANT: De Robertis, Edward M.
 ATTORNEY/AGENT INFORMATION:
 ADDRESS: Majestic, Parsons, Siebert & Hsue
 STREET: Four Embarcadero Center, Suite 1100
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94111-4106

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/878,474
 FILING DATE: 18-JUN-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/020,150
 FILING DATE: 20-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Siebert, J. Suzanne
 REGISTRATION NUMBER: 28,758
 REFERENCE/DOCKET NUMBER: 3100.002US1
 TELEPHONE: 415/248-5500
 TELEFAX: 415/362-5418
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 325 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

US-08-878-474-3

RESULT 3
 US-08-878-474-3
 Sequence 3, Application US/08878474
 Patent No. 6133232

GENERAL INFORMATION:
 APPLICANT: De Robertis, Edward M.
 ATTORNEY/AGENT INFORMATION:
 ADDRESS: Majestic, Parsons, Siebert & Hsue
 STREET: Four Embarcadero Center, Suite 1100
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94111-4106

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/878,474
 FILING DATE: 18-JUN-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/020,150
 FILING DATE: 20-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Siebert, J. Suzanne
 REGISTRATION NUMBER: 28,758
 REFERENCE/DOCKET NUMBER: 3100.002US1
 TELEPHONE: 415/248-5500
 TELEFAX: 415/362-5418
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 318 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

US-08-878-474-3

Query Match 43.4%; Score 816; DB 4; Length 318;
 Best Local Similarity 50.3%; Pred. No. 5e-73; DB 4; Length 318;
 Matches 161; Conservative 47; Mismatches 78; Indels 34; Gaps 8;

Query 22 AFCEARIPCMCHMPNITRPNLHLHSTQANALIAEQY 61

Db 29 ASCEPYRIPCKKSMPIKMMTAKMPNHLHHSTQANAILAIEQFGLLTTECSQDLFFLICAMY 88
 Qy 82 A P I C T L E F L D P T K P C K S V C O R A R D C E P L M K M Y N H S P E I A C D E P L V Y D R G Y C I S P E A 141
 Db 89 A P I C T D F Q H E P T K P C K S V C E A R A G C E P L I K Y R I T W P E S I A C E E P L P D R G V C I S P E A 148
 Qy 142 I V D L P E D V K N D I T D P M M Q E R P L D V D C K R L S P D R C K K V K P I L A T Y L S K N Y S Y V H A 201
 Db 149 I V T V E Q G T D S M P F S M D S N N G G S G R E N C K C P M K A T O K T Y K N N Y V I R A 201
 Qy 202 K I K A V O R S G C N E V T T V D V K E F K S S S P I P R T Q V P L I T I N S C O P H I L P Q D V I M C E 260
 Db 202 K V K E V - K V K C H D A T A I V E K V E K I L K S L V N I K D T V P L Y T N G C L C P Q I V A N E Y I M G Y E 260
 Qy 261 W R S R M M L E N C L V E K W D Q L S K R S T Q W E E R L Q E Q R T Y V D K K T P A G R T S R S N P P K P G 318
 Db 261 D K E R T R I L V E C S L A E K W D R I L A K K V K R W D Q L K R R P R K S K 300
 Qy 319 K P P A K P D A S P K K N I K T R S A Q 338
 Db 301 D V A P I P N N N S N S Q A R 317

RESULT 4
 ; Sequence 9, Application US/08937067
 ; Patent No. 6433155

; GENERAL INFORMATION:
 ; APPLICANT: Umansky, Hovsep
 ; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
 ; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018

; COMPUTER READABLE FORM:
 ; COMPUTER TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/937,067
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Leinhardt, Susan K.
 ; REGISTRATION NUMBER: 33,943
 ; REFERENCE/DOCKET NUMBER: 23647-20018.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 813-5600
 ; TELEFAX: (650) 494-0792
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 585 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-08-937-067-9

Qy 64 L V D V N C S A V L R F F C A M Y A P I C T L E F L D P I K P C K S V C O R A R D C E P L M K M Y N H S P E S L 123
 Db 73 L V E I Q C S P D L R F L C M T P I C L P D Y - H K P L P C R S V C E R A K G C S P L M R Q G F A P E R M 131
 Qy 124 A C D E L P V Y D R G Y C I S P E A I V T D L P E D V K W I D I T P D M M V Q E R P L D V D C K R L 173
 Db 132 S C D R L P V L G R D A E V L C M D Y N R S E A T I A P P R F P A K T L P P G P A P S G G B C P A G 185
 Qy 174 S P D R C R C R K - V K P T L A T Y L S K N Y S Y V H A K I K A V O R S G C 211
 Db 186 G P F V C K C R E P F V P I L K E S H P L Y N K V R T G Q V P N C 218

RESULT 5
 ; Sequence 14, Application US/08937067
 ; Patent No. 6433155

; GENERAL INFORMATION:
 ; APPLICANT: Umansky, Samuil
 ; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
 ; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018

; COMPUTER READABLE FORM:
 ; COMPUTER TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/937,067
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Leinhardt, Susan K.
 ; REGISTRATION NUMBER: 33,943
 ; REFERENCE/DOCKET NUMBER: 23647-20018.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 813-5600
 ; TELEFAX: (650) 494-0792
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 685 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-08-937-067-14

Qy 4 S I L V A C I L W H I L A G V R G A P C B A V R I P M C R H P W N I T R M P N H H S T O E N A I L A I 58
 Db 11 S U L A A L A V - L Q R S S G A A A S A R E L A C Q E I T V L C K G I G Y N T Y M P O F N H D T Q D E A G L E V 69

Query Match 16.28; Score 305; DB 4; Length 685;
 Best Local Similarity 39.5%; Pred. No. 7.9e-22;
 Matches 58; Conservative 31; Mismatches 46; Indels 12; Gaps 5;

Qy 5 I L V A C I L W H I L A G V R G A P - C E A V R I P M C R H P W N I T R M P N H H S T O E N A I L A I Q Y E E 63
 Db 13 L I L L A Q L V G R A A A S K A P V C Q E I T V P M C R G T G Y N L T H M P N Q F N H D T Q D E A G L E V H Q F N P 72

Query Match 18.0%; Score 338.5; DB 4; Length 585;
 Best Local Similarity 33.3%; Pred. No. 3e-25; Mismatches 84; Indels 25; Gaps 6;

Qy 59 E O Y E E L V D V N C S A V L R F F C A M Y A P I C T L E F L D P I K P C K S V C O R A R D C E P L M K M Y N H S 118
 Db 70 H O F W P L V E I Q C S P D L K F F L C S M T P I C - L E D Y K K P L P C R S V C E R A K G C A P L M R Q G F A 128

Qy 119 W E S L A C D E L P Y D R G V C I S P E A I V T D 145
 Db 129 W P D R M C D R L P - E Q G N P D T L C M D 150

RESULT 6
US-08-937-067-13
Sequence 13, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 572 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION NUMBER: US-08-937-067-8

Query Match 15.9%; Score 298.5; DB 4; Length 572;
Best Local Similarity 46.1%; Pred. No. 2.e-21;
Matches 53; Conservative 21; Mismatches 38; Indels 3; Gaps 2;

RESULT 7
US-08-937-067-8
Sequence 8, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.

Qy 24 CEAVRIPMCRHMPPNITRMPNHLHHSTQENATLAEQYEEVLVDNCASAVLREFFCAMYAP 83
Db 49 CQPISIPLCTDIAYNQTLNLNLGHNTQEDAGLEVHQPLVKVQCSPELRFLCSMVP 108
Qy 84 ICLTEFLHDPIPKCKSYCQRARDCEPILMKMNHSWPSLACDELPVYD-RVCIS-E-- 140
Db 109 VCTV--LDOAIPPCRSICERAROGCEALMNKGFGQWPERLCEHFPRHGAEQTCVGQNHS 156

Qy 141 -----AVYTDLP 147
Db 157 EDGAPALDTTAP 168

RESULT 8
US-08-937-067-10
Sequence 10, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.

Qy 24 CEAVRIPMCRHMPPNITRMPNHLHHSTQENATLAEQYEEVLVDNCASAVLREFFCAMYAP 83
Db 49 CQPISIPLCTDIAYNQTLNLNLGHNTQEDAGLEVHQPLVKVQCSPELRFLCSMVP 108
Qy 84 ICLTEFLHDPIPKCKSYCQRARDCEPILMKMNHSWPSLACDELPVYD-VCI 137
Db 109 VCTV--LDOAIPPCRSICERAROGCEALMNKGFGQWPERLCEHFPRHGAEQTCVGQNHS 161

Qy 24 CEAVRIPMCRHMPPNITRMPNHLHHSTQENATLAEQYEEVLVDNCASAVLREFFCAMYAP 83
Db 49 CQPISIPLCTDIAYNQTLNLNLGHNTQEDAGLEVHQPLVKVQCSPELRFLCSMVP 108
Qy 84 ICLTEFLHDPIPKCKSYCQRARDCEPILMKMNHSWPSLACDELPVYD-VCI 137
Db 109 VCTV--LDOAIPPCRSICERAROGCEALMNKGFGQWPERLCEHFPRHGAEQTCVGQNHS 161

Qy 24 CEAVRIPMCRHMPPNITRMPNHLHHSTQENATLAEQYEEVLVDNCASAVLREFFCAMYAP 83
Db 49 CQPISIPLCTDIAYNQTLNLNLGHNTQEDAGLEVHQPLVKVQCSPELRFLCSMVP 108
Qy 84 ICLTEFLHDPIPKCKSYCQRARDCEPILMKMNHSWPSLACDELPVYD-VCI 137
Db 109 VCTV--LDOAIPPCRSICERAROGCEALMNKGFGQWPERLCEHFPRHGAEQTCVGQNHS 161

Qy 54 AILAEQYBELLVDVNCASVLRFFPCAMYAPICITLEFLHDPIKPCSKYCQRADDCEPLMK 113
 Db 70 AIQOSSSWLPLARECHPARDIFLCSLEAPICPDRY----IFICRSLGCAVRSSCAPIMA 125

Qy 114 MYNHSPWESLACDELPVYDRGCVISPEAIVTDLPEDVKWIDITPDMAYQERPLDVDCRKL 173
 Db 126 CYGPWPPEIPLKCDKF-EDGMICIS---TTN-----DTGSTRR 160

Qy 174 SPDRCKCKVY-----KPLATYLSKNYSYTHAKIKAVOR--SGCNEVTVTVDVKEIFKSSSPIP--RTQVP--LTNTS 241
 Db 161 TVPRASCRDCELEBGSTSKEILOTFCHNDVF---AKYRITKKNITSANLYDFDLSKLE 216

Qy 223 IFKSS-----PIPRTOVPLINSSCO-----CPHILPHQDVLMCYEWSR 263
 Db 217 ILKGSLPKTDVLPLRQQWLDDATCVQNMIMRGTRTGVVYICAEVGKVVNNAYAMQK 276

RESULT 11
 Qy 264 RMLLENCLVEKWD 278
 Db 277 KNKNL-HFAVRKWKN 290

RESULT 12
 Qy 265 Sequence 2, Application US/08893654B
 Db 278 GENERAL INFORMATION:
 ; APPLICANT: RACIE, LISA, ET ALIA
 ; TITLE OF INVENTION: Frazzled NUCLEOTIDE SEQUENCES,
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENETICS INSTITUTE, INC.
 ; STREET: 87 CAMBRIDGE PARK DRIVE
 ; CITY: CAMBRIDGE
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02140-2387
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/893,654B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/893,654B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MEINERT, M.C.
 ; REGISTRATION NUMBER: 31,544
 ; REFERENCE/DOCKET NUMBER: G1 5279
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-498-8574
 ; TELEX/FAX: 617-876-5851
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ;
 ; Query Match 12.4%; Score 232.5; DB 4; Length 281;
 ; Best Local Similarity 24.0%; Pred. No. 3.7e-15;
 ; Matches 69; Conservative 44; Mismatches 101; Indels 73; Gaps 13;

Qy 21 GAPCEAVRIP----MCRHMPWNTRMPNHLHSTQENALAIQEYELVDVNCASVLRFF 76
 Db 22 GLSTPKCVPKEMACNDGYSEMRLPNLGHNTMAEVVPSKSAEWQNLJQTGHPYARTF 81

Qy 77 FCAMYAPICITLEFLHDPIKPCSKYCQRADDCEPLMKMYNSKSPESLACDELPVYDRGVC 136
 Db 82 LCSELFAPIVCLDTF---TOPCRSMCVAVRNSCAPVLAHGHSMPESLDCDRFPAGE--- 133

Qy 137 ISPEAVITDLPEDVKWIDITPDMMVQERPLDVDCRKLSDPDRCK-CKVY-----KPTLAT 189
 Db 134 -----DNLDTLSKE--YQAYAKELPKSCCGCPILIEFFSHKTVEA 174

Qy 190 YLSKKNYSYVIHAKIKAVOR--SGCNEVTVTVDVKEIFKSSSPIP--RTQVP--LTNTS 241
 Db 175 FCDNFA ---VKVLAKKTTSGLHEYETEGPV-EFIKGULLPYDTRTMIEQWLLINE 229

Qy 242 SCQCPHI-----LPHODVLMCYEWSRSMMLLENCLVEKW 276
 Db 230 NCAQKLIRNRPTVYVIAGDINGKIKFC-----SPCVLREW 266

RESULT 12
 Qy Sequence 4, Application US/08893654B
 ; Patent No. 6165748
 ; GENERAL INFORMATION:
 ; APPLICANT: RACIE, LISA, ET ALIA
 ; TITLE OF INVENTION: Frazzled NUCLEOTIDE SEQUENCES,
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENETICS INSTITUTE, INC.
 ; STREET: 87 CAMBRIDGE PARK DRIVE
 ; CITY: CAMBRIDGE
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02140-2387
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/893,654B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MEINERT, M.C.
 ; REGISTRATION NUMBER: 31,544
 ; REFERENCE/DOCKET NUMBER: G1 5279
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-498-8574
 ; TELEX/FAX: 617-876-5851
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 280 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ;
 ; Query Match 12.2%; Score 228.5; DB 4; Length 280;
 ; Best Local Similarity 23.9%; Pred. No. 9.1e-15;
 ; Matches 69; Conservative 45; Mismatches 110; Indels 65; Gaps 13;

Qy 21 GAPOEAVRIP----MCRHMPWNTRMPNHLHSTQENALAIQEYELVDVNCASVLRFF 76
 Db 21 GLSTPKCVPKEMACNDGYSEMRLPNLGHNTMAEVVPSKSAEWQNLJQTGHPYARTF 80

Qy 77 FCAMYAPICITLEFLHDPIKPCSKYCQRADDCEPLMKMYNSKSPESLACDELPVYDRGVC 136
 Db 81 LCSLFAPIVCLDTF---TOPCRSMCVAVRNSCAPVLAHGHSMPESLDCDRFPAGE--- 132

Qy 137 ISPEAVITDLPEDVKWIDITPDMMVQERPLDVDCRKLSDPDRCK-CKVY-----KPTLAT 189
 Db 133 -----DNLDTLSKE--YQAYAKELPKSCCGCPILIEFFSHKTVEA 173

Qy 190 YLSKKNYSYVIHAKIKAVOR--SGCNEVTVTVDVKEIFKSSSPIP--RTQVP--LTNTS 241
 Db 174 FCDNFA ---VKVLAKKTTSGLHEYETEGPV-EFIKGULLPYDTRTMIEQWLLINE 228

RESULT 14
US-08 987-289-2 ; Sequence 2, Application US/08987289
; Patent No. 5934098
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A Human 7-TM Receptor Similar
; to Murine Frizzled-6 gene

RESULT 13
US-08-937-067-7 ; Sequence 7, Application US/08937067
; Patent No. 643155
; GENERAL INFORMATION:
; APPLICANT: Umnatsky, Samuil
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES: PEPTIDES ENCODED THEREBY AND
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE: (650) 813-5560
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 3,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 494-0792
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-987-289-2

Query Match 11.7%; Score 220; DB 2; Length 706;
Best Local Similarity 31.9%; Pred. No. 2.3e-13;
Matches 44; Conservative 27; Mismatches 63; Indels 4; Gaps 3;

Qy 1 MFLSIVIYALCILWHLAIGVRGAPCEAVRIPCMGRMPWNITRMPNHLHSTOBNAIAIEQ 60
Db 3 MFTFLLT-CIFPLPLRGHSLEFTCEPITVPRCMKMYNMTFPNLGHYDOSTAAVEMEH 60

Query Match 11.7%; Score 220; DB 2; Length 706;
Best Local Similarity 31.9%; Pred. No. 2.3e-13;
Matches 44; Conservative 27; Mismatches 63; Indels 4; Gaps 3;

Qy 61 YEEELVDVNCASAVLRFPCAMYAPICTLEFLDPKPSVYCORARDCEPLMKMNHNSWP 120
Db 61 FLPLANECLCSPNIEFLCKAFVPTCIEQIH-VVPCKRLCEKVYSPCKKLIDTFCIRWP 118

Query Match 11.7%; Score 220; DB 2; Length 706;
Best Local Similarity 31.9%; Pred. No. 2.3e-13;
Matches 44; Conservative 27; Mismatches 63; Indels 4; Gaps 3;

Qy 121 ESLACDELPVYDRGCYTS 138
Db 119 EEECDRLQYCDETVPPV 136

RESULT 15
US-08-937-067-2 ; Sequence 2, Application US/08937067
; Patent No. 643155
; GENERAL INFORMATION:
; APPLICANT: Umnatsky, Samuil
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF

RESULT 16
US-08-937-067-2 ; Sequence 2, Application US/08937067
; Patent No. 643155
; GENERAL INFORMATION:
; APPLICANT: Meltonyan, Horsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF

Query Match 12.1%; Score 228; DB 4; Length 314;
Best Local Similarity 26.3%; Pred. No. 1.2e-14;
Matches 72; Conservative 45; Mismatches 107; Indels 50; Caps 14;

Qy 23 PCEAVRIP---MCRHMPWNITRMPNHLHSTQENAILAEQEYELDVNCASAVLREFFC 78
Db 55 PFQCVDP1PADLRLCHNYGYKKMVLPNLLEHTMAEVQKQASSWPLNKCHAGTQVFLC 114

Query Match 12.1%; Score 228; DB 4; Length 314;
Best Local Similarity 26.3%; Pred. No. 1.2e-14;
Matches 72; Conservative 45; Mismatches 107; Indels 50; Caps 14;

Qy 79 AMYAPICTLEFLDPKPKCSVQCARDDCEPLMKMNHNSWPESACDELPVYDRGCYTS 138
Db 115 SLFAPVC---LDRPIYPCKRWCIVAEYRDSCCEPMQFFGFYPMEMLKCDKFPEGD--VCIA 168

Query Match 12.1%; Score 228; DB 4; Length 314;
Best Local Similarity 26.3%; Pred. No. 1.2e-14;
Matches 72; Conservative 45; Mismatches 107; Indels 50; Caps 14;

Qy 139 ---PEAIVTDLPEVDWKIDTPDMAYQERPLDVDCRKLSPDRCKKKVPTLATYLSKVN 195
Db 169 MTPPNPTEASRPGT---TVCP-----PCDNELK-----SEALIEHUCAS- 205

Query Match 12.1%; Score 228; DB 4; Length 314;
Best Local Similarity 26.3%; Pred. No. 1.2e-14;
Matches 72; Conservative 45; Mismatches 107; Indels 50; Caps 14;

Qy 196 SYVIHAKIKAVYORGSCNEVTTVVDYKEIKSSSPTRTOV-----LITNSSCOPHI- 248
Db 206 EFALRMKTKYKEKE--NGDKIVPKKKPKLKGPKKKDRLKLVLYLKNGADCPCHOLDNN 263

Query Match 12.1%; Score 228; DB 4; Length 314;
Best Local Similarity 26.3%; Pred. No. 1.2e-14;
Matches 72; Conservative 45; Mismatches 107; Indels 50; Caps 14;

Qy 249 LPHQDVLMICYEWSRNMMLNCLVKWQDLSK 282
Db 264 LSHH-FLIMGRKVKSQYL--TAIHKW-DRKKN 292

```

; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-937-067-2

```

```

Query Match          11.6% Score 218; DB 4; Length 295;
Best Local Similarity 26.3%; Pred. No. 1.le-13;
Matches 62; Conservative 41; Mismatches 91; Indels 42; Gaps 9;
Qy      6 LVALCLWLHLAGC-----VRGAPCEAVRIPMCRHMPNTI-----TRMPNHLHS 49
Db      8 LLLVLVASHCUGLSARGLFLFGOPDFSKYKRTCKPINAQLCHGEYQNRLPNLNLGE 67
Qy      50 TQENAILAEYEELEYDYNCAVLRFFCAMAYAPICLLEFLHDPIPKCKSYCORARDCE 109
Db      68 TMEKEVLQAGANIPLYMKQCHPTKKELCSLFAVPC-LDDLDETIQFCHSCLCVQVKDRCA 126
Qy      110 PLMKMYNHISWPESLACDELPIVYDRGYCISPEALIVTDPEYKWDITTPDMAYQERPLDVD 169
Db      127 PVMSAFGFPWPDMLECDRFP-QDNDLCLPLASSDHLLP-----ATEEARKVCE 173
Qy      170 -CKRLSPD----RCCK-----KVKTPLATYLSKNSVYTHAKIKAVQR-SGCNE 213
Db      174 ACKTKNEDDDNIDMETLCKNDALKIKYKEITTYINRDTKILETKSITYKLVNGVSE 229

```

Search completed: March 7, 2003, 11:25:47
Job time : 17 secs

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OM protein - protein search, using sw model

Run on: March 7, 2003, 11:21:34 ; Search time 20 Seconds
(without alignments)
1663.126 Million cell updates/sec

Title: US-09-909-775-2
Perfect score: 1879
Sequence: MFLSTLVALCLWLHALGVR.....SPKKNIKTRSAQKRTNPKRV 346

Scoring table: BL05UR62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:
1: pir1:
2: pir2:
3: pir3:
4: pir4:
.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1033	55.0	197	JC7735	frizzled-related protein wingless receptor
2	319	17.0	694	JE0178	Frizzled-1 protein probable intercell
3	300.5	16.0	647	JE0137	Frizzled-7 protein
4	300	16.0	641	A45054	Frizzled-2 protein
5	298.5	15.9	574	JE0139	gene frizzled protein
6	293	15.6	565	SO3348	Frizzled-1 protein
7	289	15.4	581	SO3340	FZD10 protein - human wingless protein receptor
8	283	15.1	568	T25162	Frizzled-6 protein
9	282	15.0	581	JC7086	Frizzled Protein 4
10	279	14.8	530	T37325	frizzled-3 protein
11	265	14.1	537	JC7127	hypothesised protein
12	262.5	14.0	666	JC7312	low-density lipoprotein membrane-type frizzled protein-1
13	226.5	12.1	605	T3190	collagen alpha 1(X)
14	220	11.7	706	JE0164	frizzled protein-2
15	218	11.6	295	JE0174	frizzled protein-2
16	207	11.0	317	JE0175	membrane-type frizzled protein-1
17	204	10.9	1113	JE0115	hypothesised protein
18	162	8.6	579	JC7629	hypothesised protein
19	149	7.9	1774	B56101	hypothesised protein
20	120.5	6.4	526	T13484	hypothesised protein
21	107	5.7	400	T46383	hypothesised protein
22	107	5.7	3488	T34418	hypothesised protein
23	106.5	5.7	651	T21175	hypothesised protein
24	105	5.6	793	JC5539	smoothened protein
25	103.5	5.5	965	S62935	hypothesised protein
26	98.5	5.2	492	F8684	probable protein
27	96.5	5.1	581	B54665	neuin-2 precursor
28	96.5	5.1	1483	E86143	F653.12 protein
29	94.5	5.0	606	A54665	neuin-1 precursor

ALIGNMENTS

RESULT 1						
JC7735	frizzled-related protein - rat					
C:Species: Rattus norvegicus (Norway rat)						
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 *text_change 14-Dec-2001						
C:Accession: JC7735						
R.Yam, J.W.P.; Chan, K.W.; Wong, V.K.W.; Hsiao, W.L.W.						
Biochem. Biophys. Res. Commun. 286, 94-100, 2001						
A:Title: Transcriptional activity of the promoter region of rat frizzled-related protein						
A:Reference number: JC7735; PMID:21378144; PMID:11495313						
A:Accession: JC7735						
A:Molecule type: DNA						
A:Residues: 1-197 <YAM>						
A:Cross references: GB:AF140347						
C:Comment: This protein is a new family of secreted proteins involved in tumorigenes.						
C:Genetics:						
A:Gene: rfrp						
A:Introns: 148/3; 175/3						
Query Match Score 55.0%; Best Local Similarity 94.9%; Matches 187; Conservative 1; Mismatches 9; Indels 0; Gaps 0;						

A; Molecule type: DNA <BHA>
A; Cross-references: ENBL:U65589
A; Note: mRNA was also sequenced submitted to the EMBL Data Library, July 1996
A; Reference number: S78444
A; Accession: S78444
A; Molecule type: DNA
A; Residues: 1-416, 'T' 418-594 <BHW>
C; Genetics:
A; Gene: dfz2
A; Cross-references: FlyBase:FBgn0016797
C; Keywords: transmembrane protein
C; Superfamily: fruit fly frizzled protein

Query Match 17.0% Score 319; DB 2; Length 694;
Best Local Similarity 38.3%; Pred No. 5.9e-18;
Matches 59; Conservative 25; Mismatches 40; Indels 30; Gaps 3;

Qy 18 GYRGAP-----CEAVTIPCMCRHMPWNTRIMNLHISTONAILATEEQYEELVDYINC 71
Db 52 GVAIPKDNPRLBEITIPCMRCIGYNTSFNEMNETQDAGLEYHOFLVLEIKCSP 111

Qy 72 VLRFFFCAMYAPICLTLEFLHDPTKPKCSVCQRARDCEPLAKMKNHSWPESLACDELPVY 131
Db 112 DLKKFLCLSMYTPTIC-LEDYHKPLPVCRSVCEARSGGAPIQQYSFWPERMACHEILPLH 170

Qy 132 DRGVYCISPEATIVTDLPEDVKWIDTPDMVQERP 165
Db 171 G-----DPDNLCMEQP 181

RESULT 3
JE0337 Frizzled-1 protein - human
C; Species: Homo sapiens (man)
C; Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C; Accession: JE0337
R; Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A; Title: Molecular cloning, differential expression, and chromosomal localization of human Frizzled-1 protein
A; Reference number: JE0337; PMID:99032814; PMID:9813155
A; Accession: JE0337
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-647 <SGA>
A; Cross-references: DDBJ:AB017363; NID:93927882; PID:BAAA34666.1; PMID:93927883
C; Superfamily: fruit fly frizzled protein

Query Match 16.0% Score 300.5; DB 2; Length 647;
Best Local Similarity 45.5%; Pred No. 1.7e-15;
Matches 52; Conservative 25; Mismatches 35; Indels 3; Gaps 2;

Qy 24 CEAIRPMCRHMWNTRMPNLHSTQENAILATEEQYEELVDYINC 83
Db 116 COPISIPLCTDIAYNOTIMPNLIGHTNOEDAGLEYHOFLVQCSAELREFLCSMYAP 175

Qy 84 ICITLEFLHDPTKPKCSVCQRARDCEPLAKMKNHSWPESLACDELPVYDRG-VCI 137
Db 176 VCTV--LEQALPPCRSLCERARQCEALMNKGFGQWPDTLKECKFPYHGAELCV 228

RESULT 4
A45054 probable intercellular signal transducer or transmitter Fz-1 - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 02-Mar-2001
A; Accession: A45054
R; Chan, S. D.; Karpf, D. B.; Fowlkes, M. E.; Hooks, M.; Bradley, M.S.; Vuong, V.; Bambino, J. Biol. Chem. 267, 25202-25207, 1992
A; Title: Two homologs of the *Drosophila* polarity gene *frizzled* (fz) are widely expressed

A; Reference number: A45054; MUID:93094228; PMID:1334084
A; Accession: A45054
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-641 <CHAD>
A; Experimental source: UMR 106 osteosarcoma cell line
A; Note: sequence extracted from NCBI backbone (NCBIP:120154)
C; Superfamily: fruit fly frizzled protein

Query Match 16.0% Score 300; DB 2; Length 641;
Best Local Similarity 36.5%; Pred No. 1.9e-16;
Matches 62; Conservative 26; Mismatches 38; Indels 44; Gaps 5;

Qy 9 LCIWL--HLAGVVRGAP-----CEAVR 28
Db 56 LLWILLEAPLLGVRAQAGQVSGPGQRPPPQPGQQYNGERCISIDPHGYCCPIS 115

Qy 29 I TPMCRHMWNTRMPNLHSTQENAILATEEQYEELVDYINC 88
Db 116 I PLCTDIAYNOTIMPNLIGHTNOEDAGLEYHOFLVQCSAELREFLCSMYAPCTV- 174

Qy 89 FLHDPIPKCSVCQRARDCEPLAKMKNHSWPESLACDELPVYDRG-VCI 137
Db 175 -LEQALPPCRSLCERAO-GCEALMNKGFGQWPDTLKECKFPVHGRGELCV 222

RESULT 5
JE0339 Frizzled-7 protein - human
C; Species: Homo sapiens (man)
C; Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C; Accession: JE0339
R; Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A; Title: Molecular cloning, differential expression, and chromosomal localization of human Frizzled-7 protein
A; Reference number: JE0337; PMID:99032814; PMID:9813155
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-574 <SGA>
A; Cross-references: DDBJ:AB017365; NID:93927886; PID:BAAA34668.1; PMID:93927887
C; Accession: JE0339
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-574 <SGA>
A; Cross-references: DDBJ:AB017365; NID:93927886; PID:BAAA34668.1; PMID:93927887
C; Accession: JE0339
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-574 <SGA>
A; Cross-references: DDBJ:AB017364; NID:93927886; PID:BAAA34667.1; PMID:93927885
C; Accession: JE0339
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-565 <SGA>
A; Cross-references: DDBJ:AB017364; NID:93927886; PID:BAAA34667.1; PMID:93927885
C; Superfamily: fruit fly frizzled protein

Query Match 15.9% Score 298.5; DB 2; Length 574;
Best Local Similarity 46.1%; Pred No. 2.2e-16;
Matches 53; Conservative 21; Mismatches 38; Indels 3; Gaps 2;

Qy 24 CEAIRPMCRHMWNTRMPNLHSTQENAILATEEQYEELVDYINC 83
Db 49 CQPISIPLCTDIAYNOTIMPNLIGHTNOEDAGLEYHOFLVQCSPELREFLCSMYAP 108

Qy 84 ICITLEFLHDPIPKCSVCQRARDCEPLAKMKNHSWPESLACDELPVYDRG-VCI 137
Db 109 VCTV--LDQAIQPCRSLCEARQCEALMNKGFGQWPDTLKECKFPVHGRGELCV 161

RESULT 6
JE0338 Frizzled-2 protein - human
C; Species: Homo sapiens (man)
C; Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C; Accession: JE0338
R; Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A; Title: Molecular cloning, differential expression, and chromosomal localization of human Frizzled-2 protein
A; Reference number: JE0337; PMID:99032814; PMID:9813155
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-565 <SGA>
A; Cross-references: DDBJ:AB017364; NID:93927886; PID:BAAA34667.1; PMID:93927885
C; Superfamily: fruit fly frizzled protein

Query Match 15.68; Score 293; DB 2; Length 565;
 Best Local Similarity 41.78; Pred. No. 6e-16;
 Matches 55; Conservative 22; Mismatches 45; Indels 10; Gaps 3;

Qy 24 CEAVERIPMCRRMPWNITRMPNHLHHSTQENAILATEQYEVLVDVNCASAVLRFCCAMYAP 83
 Db 39 CQPISPLPCTDIAVNQTIMPNLIGHTNQEDAGLEPHQFVVKVQCSPELREFLCSMYAP 98

Qy 84 ICTLFLHDPPIPKCKSVQRARDCEPLMKMHNHSWPESLACDELPLPVYD-RGVCTISP-- 140
 Db 99 VCTV--LEQAAPPCCRSCICERARQGCBALMNKKFGFQWPERLRCHEPRHGAEQICVGQNHS 156

Qy 141 -----ALVTDLIP 147
 Db 157 EDGAPAAILTAP 168

R; Wild, A.
 submitted to the EMBL Data Library, October 1996
 A; Reference number: Z19989
 A; Accession: "T25162
 A; Status: preliminary; translated from GB/EMBL/DDJB
 A; Molecule type: DNA
 A; Residues: 1-568 <WIL>
 A; Cross-references: EMBL:281128; PIDN:CAE03398.1; GSPDB:GN00019; CESP:T23D8.1
 A; Experimental source: clone T23D8
 R; Rocheleau, C.E.; Downs, W.D.; Lin, R.; Wittmann, C.; Bei, Y.H.; Ali, M.; P
 Cell 90, 707-716, 1997
 A; Title: Wnt signalling and an APC related gene specify endoderm in early *C. elegans*
 A; Reference number: z15051; MUID: 97433081; PMID: 9288750
 A; Accession: T42210
 A; Status: preliminary; translated from GB/EMBL/DDJB
 A; Molecule type: mRNA
 A; Residues: 1-568 <ROC>
 A; Cross-references: EMBL:AF013953; NID:92463673; PIDN:AAC47750.1; PID:92463674

RESULT 7

S03540 gene frizzled protein precursor - fruit fly (*Drosophila melanogaster*)
 C; Species: *Drosophila melanogaster*
 C; Date: 31-Mar-1990 *sequence_revision 31-Mar-1990 #text_change 02-Mar-2001
 C; Accession: S03540; S15708; S15709
 R; Vinson, C.R.; Conover, S.; Adler, P.N.

A; Title: A *Drosophila* tissue polarity locus encodes a protein containing seven potential
 A; Reference number: S03540; MUID: 89459415; PMID: 293583

A; Accession: S03540
 A; Status: not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 1-581 <VN>
 R; Adler, P.N.; Vinson, C.; Park, W.J.; Conover, S.; Klein, L.
 Genetics 126, 401-416, 1990

A; Title: Molecular structure of frizzled, a *Drosophila* tissue polarity gene.
 A; Reference number: S15708; MUID: 91060073; PMID: 2174014
 A; Accession: S15708

A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-581 <ADL>

A; Cross-references: EMBL:K54648; NID:97973; PIDN:CAA38460.1; PID:9804979

A; Accession: S15709
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-405, 'MI', 408, 'WQFHTIN' <AD2>
 A; Cross-references: EMBL:K54648; NID:97973; PIDN:CAA38461.1; PID:9804980

A; Gene: FlyBase:fz
 A; Cross-references: FlyBase:FBg0001085
 C; Keywords: fruit fly frizzled protein
 F; 1-26/Domain: signal sequence #status predicted <STG>
 F; 27-581/Product: gene frizzled protein #status predicted <STG>

Query Match 15.48; Score 289; DB 2; Length 581;
 Best Local Similarity 44.08; Pred. No. 1.3e-15;
 Matches 51; Conservative 27; Mismatches 34; Indels 4; Gaps 3;

Qy 24 CEAVERIPMCRRMPWNITRMPNHLHHSTQENAILATEQYEVLVDVNCASAVLRFCCAMYAP 83
 Db 53 CRPITISCKNPYNNMPNLPNLIGHTNQEDAGLEPHQFVVKVQCSPELREFLCSLYP 112

Qy 84 ICTLFLHDPPIPKCKSVQRARDCEPLMKMHNHSWPESLACDELPLPVYD-RGVCTISP 138
 Db 113 VCTI--LERPIPCCRSCICERARQGCBALMNKKFGFQWPERLRCHEPRHGAEQICVGQNHS 165

R; Wild, A.
 submitted to the EMBL Data Library, October 1996
 A; Reference number: Z19989
 A; Accession: "T25162
 A; Status: preliminary; translated from GB/EMBL/DDJB
 A; Molecule type: DNA
 A; Residues: 1-568 <WIL>
 A; Cross-references: EMBL:281128; PIDN:CAE03398.1; GSPDB:GN00019; CESP:T23D8.1
 A; Experimental source: clone T23D8
 R; Rocheleau, C.E.; Downs, W.D.; Lin, R.; Wittmann, C.; Bei, Y.H.; Ali, M.; P
 Cell 90, 707-716, 1997
 A; Title: Wnt signalling and an APC related gene specify endoderm in early *C. elegans*
 A; Reference number: z15051; MUID: 97433081; PMID: 9288750
 A; Accession: T42210
 A; Status: preliminary; translated from GB/EMBL/DDJB
 A; Molecule type: mRNA
 A; Residues: 1-568 <ROC>
 A; Cross-references: EMBL:AF013953; NID:92463673; PIDN:AAC47750.1; PID:92463674

RESULT 8

T25162 Frizzled-1 protein homolog - *Caenorhabditis elegans*
 C; Species: *Caenorhabditis elegans*
 C; Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 #text_change 02-Mar-2001
 C; Accession: T25162; T42210

A:Cross-references: EMBL:AF016413; PIDN:AAB65257.1; GSPDB:GN00023; CESP:F27E11.3
 A:Experimental source: strain Bristol N2; clone F27E11
 C:Genetics:

A:Gene: CESP:F27E11.3

A:Map position: 5 454/1; 520/1; 562/1
 C:Superfamily: fruit fly frizzled protein

Query Match 12.1%; Score 226.5; DB 2; Length 605;
 Best Local Similarity 29.5%; Pred. No. 1. 6e-10;
 Matches 59; Conservative 27; Mismatches 77; Indels 37; Gaps 7;
 Qy 39 ITTRMPNHILHSTQONNALIAEQQEELVDYDNCASAVLRFFFCAMYAPICLTFLHDPTIKPKCK 98
 Db 1 MTSFPNSYGHXQEAEGLVHDFYPLVEGCRQLKEFLCTMYPICQ-ENYDKPILPCM 59
 Qy 99 SWCQRARDDCEPLMKMYNHNPESLACDLP-----VYDRGVCISPEAIVTDLPLP-----147
 Db 60 ELCVEARKSCPSIMAKYGRNPETLSCEALKMSDMSTGNCAAP----PDTPKKQHKKG 115
 Qy 148 -----EDVKWIDITPPDMVQERPLDVDCRKSPDRCKKKVP-----TTLATVLSK 193
 Db 116 HHHKQNQNQNQNQNHNNSPDGPVEVGISKIDNEVIA--GPSECQCTCNQPFQVASEKSKV 172
 Qy 194 ---NVSYVTHAKIKAVORS 209
 Db * 173 GNVTCNASCSPALAESHS 192

RESULT 14

frizzled-6 protein precursor - human
 C:Species: Homo sapiens (man)

C:Accession: JE0164

Ri:Tokunara, M.; Hirai, M.; Atoml, Y.; Terada, M.; Katoh, M.
 Biochem. Biophys. Res. Commun. 243, 622-627, 1998

A:Title: Molecular cloning of human frizzled-6

A:Reference number: JE0164; MUID:98153814; PMID:9480858

A:Molecule type: mRNA

A:Residues: 1-706 <Tok>

C:Comment: This protein is receptor for selected glycoproteins in development and carcinogenesis;

A:Gene: Hfz6

A:Map Position: 8q22.3-q23.1

C:Superfamily: fruit fly frizzled protein

C:Keywords: glycoprotein

F:1-1B/Domain: signal sequence #status predicted <SIG>

F:201-222/Domain: transmembrane #status predicted <TM1>

F:281-312/Domain: transmembrane #status predicted <TM2>

F:322-345/Domain: transmembrane #status predicted <TM3>

F:370-393/Domain: transmembrane #status predicted <TM4>

F:417-436/Domain: transmembrane #status predicted <TM5>

F:473-495/Domain: transmembrane #status predicted <TM6>

F:38,352/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.7%; Score 220; DB 2; Length 706;
 Best Local Similarity 31.9%; Pred. No. 6. 4e-10;
 Matches 44; Conservative 27; Mismatches 63; Indels 4; Gaps 3;

Qy 1 MFLSILVALCLMLHHLAIGVRGAPCEAVRTPCRHMWNTRMPNLHHSSTQENALIEQ 60

Db 3 MFTPLLT-CIPLPLRGHSLPTCEPITPRMCKMAYNTMFPNLGHYDOSIAAVEMEH 60

Qy 61 YEELVDYDNCASAVLRFFFCAMYAPICLTFLHDPTIKPKCKSQRARDDCPCEPLMKMYNHNSWP 120

Db 61 FPLPLANIECSPTNIEFLCKAFVPTC-IEQIH-VVPPCRKLCERVSDCKKLIDTFGTIRMP 118

Qy 121 ESLACDELPVDRGVCLIS 138

A:Cross-references: EMBL:AF016413; PIDN:AAB65257.1; GSPDB:GN00023; CESP:F27E11.3

A:Experimental source: strain Bristol N2; clone F27E11

C:Genetics:

A:Gene: CESP:F27E11.3

A:Map position: 5 454/1; 520/1; 562/1

C:Superfamily: fruit fly frizzled protein

Query Match 12.1%; Score 226.5; DB 2; Length 605;
 Best Local Similarity 29.5%; Pred. No. 1. 6e-10;
 Matches 59; Conservative 27; Mismatches 77; Indels 37; Gaps 7;

Qy 39 ITTRMPNHILHSTQONNALIAEQQEELVDYDNCASAVLRFFFCAMYAPICLTFLHDPTIKPKCK 98

Db 1 MTSFPNSYGHXQEAEGLVHDFYPLVEGCRQLKEFLCTMYPICQ-ENYDKPILPCM 59

Qy 99 SWCQRARDDCEPLMKMYNHNPESLACDLP-----VYDRGVCISPEAIVTDLPLP-----147

Db 60 ELCVEARKSCPSIMAKYGRNPETLSCEALKMSDMSTGNCAAP----PDTPKKQHKKG 115

Qy 148 -----EDVKWIDITPPDMVQERPLDVDCRKSPDRCKKKVP-----TTLATVLSK 193

Db 116 HHHKQNQNQNQNQNHNNSPDGPVEVGISKIDNEVIA--GPSECQCTCNQPFQVASEKSKV 172

Qy 194 ---NVSYVTHAKIKAVORS 209

Db * 173 GNVTCNASCSPALAESHS 192

RESULT 15

frizzled-6 protein precursor - human

C:Species: Homo sapiens (man)

C:Accession: JE0164

Ri:Hirai, M.; Atoml, Y.; Terada, M.; Katoh, M.
 Biochem. Biophys. Res. Commun. 243, 622-627, 1998

A:Title: Molecular cloning of human frizzled-6

A:Reference number: JE0164; MUID:98153814; PMID:9480858

A:Molecule type: mRNA

A:Residues: 1-706 <Tok>

C:Comment: This protein is receptor for selected glycoproteins in development and carcinogenesis;

A:Gene: Hfz6

A:Map Position: 8q22.3-q23.1

C:Superfamily: fruit fly frizzled protein

C:Keywords: glycoprotein

F:1-1B/Domain: signal sequence #status predicted <SIG>

F:201-222/Domain: transmembrane #status predicted <TM1>

F:281-312/Domain: transmembrane #status predicted <TM2>

F:322-345/Domain: transmembrane #status predicted <TM3>

F:370-393/Domain: transmembrane #status predicted <TM4>

F:417-436/Domain: transmembrane #status predicted <TM5>

F:473-495/Domain: transmembrane #status predicted <TM6>

F:38,352/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.7%; Score 220; DB 2; Length 706;

Best Local Similarity 31.9%; Pred. No. 6. 4e-10;

Matches 44; Conservative 27; Mismatches 63; Indels 4; Gaps 3;

Qy 1 MFLSILVALCLMLHHLAIGVRGAPCEAVRTPCRHMWNTRMPNLHHSSTQENALIEQ 60

Db 3 MFTPLLT-CIPLPLRGHSLPTCEPITPRMCKMAYNTMFPNLGHYDOSIAAVEMEH 60

Qy 61 YEELVDYDNCASAVLRFFFCAMYAPICLTFLHDPTIKPKCKSQRARDDCPCEPLMKMYNHNSWP 120

Db 61 FPLPLANIECSPTNIEFLCKAFVPTC-IEQIH-VVPPCRKLCERVSDCKKLIDTFGTIRMP 118

Qy 121 ESLACDELPVDRGVCLIS 138

Query completed: March 7, 2003, 11:25:27

Job time : 23 secs

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FT DOMAIN	33	150	FZ.	
FT DOMAIN	165	294	NTR.	
FT SITE	301	318	SER-RICH.	
FT CARGOHD	49	49	N-LINKED (GLCNAC, . .) (POTENTIAL).	
FT CARGOHD	299	299	N-LINKED (GLCNAC, . .) (POTENTIAL).	
FT CARGOHD	399	399	N-LINKED (GLCNAC, . .) (POTENTIAL).	
SQ SEQUENCE	325 AA:	36234 MN:	39B337A9C6E9BB3 CRC64;	
Query Match	44.2%	Score 831;	DB 1;	Length 325;
Best Local Similarity	51.4%	Score 831;	DB 1;	Length 325;
Matches 166; Conservative 48; Mismatches 77; Indels 32; Gaps 8;				
Qy 3 LSLIVVALCLWLHALGVGAPACEAVRIPMCRRMPWNTRMPNHLHSTQENAATLAEQEY 62				
Db 16 LLALAALCL-LRVP-GARAACEPVRIPLCKSFLPNWMTKMPNHLHSTQANAATLAEQEY 73				
Qy 63 ELVDYNGCSAVLRLPEFCAMAYAPICITLEFHDPDKPKCSVQGRADDCPEIMKMYNHSSWES 122				
Db 74 GLJGTHCSPDLLFLCPAMAYAPICITLEFHDPDKPKCSVQGRQCEPLIKYRHSWES 133				
Qy 123 LACDELPVYDGRGCISPEIAVLT---DLPEDVKWIDITPDMMVQERPLDVDDCKRLSPDRC 178				
Db 134 LACDELPVYDGRGCISPEIAVLTADGDFMDSS-----NGNCRGASSERC 178				
Qy 179 KCKKVKPPTLAYLSKNSVYVIAHKAVQRSGNEVVTVVDEWEIKFSS-SPIPLRTQVPL 237				
Db 179 KCKPVYRATQKTYFRNNYNYVTRAKVKEI-KTKCHDVTAVKEILKASLNVNPRETNL 237				
Qy 238 ITNSSCQPHILPHQDLYMCC-EWRSSMMIENCLYEKWRDOLSKRSKSIONWERLQQR 295				
Db 238 YTQSDCLCPNLYVEYLIMGYDEBBERSRLLVEGSAEKWKDRGKVKRWDMLKRHLG 297				
Qy 296 RTVQD-----KKKTAGRTSRS 311				
Db 298 LNTSSDSSHSDSTQSQQKPGRNNS 320				
RESULT 2				
ID FRZB_MOUSE	STANDARD;	PRT;	323 AA.	
AC P97093; 00907;	009093;			
DT 16-OCT-2001 (Rel. 40, Created)				
DT 16-OCT-2001 (Rel. 40, Last sequence update)				
DE Frizzled-related protein precursor (Frzb-1) (Frizzled)				
DE (Secreted frizzled related sequence protein 3) (sFRP-3).				
GN FRZB OR FRZB1 OR FBE OR SFRP3.				
OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090;				
RN SEQUENCE FROM N.A.				
RP MEDLINE=97236495; PubMed=9118218;				
RA Leyns L., Boumester T., Kim S.H., Piccolo S., De Robertis E.M.;				
RT "Frz-1 is a secreted antagonist of Wnt signaling expressed in the Spemann organizer"; Cell 88:747-756 (1997).				
RL [4]				
RP SEQUENCE FROM N.A.				
RA Mayr T., Deutsch U., Kuehl M., Drexlter H.C.A., Lottspeich F., Deutscher P., Boumester T., Kim S.H., Piccolo S., De Robertis E.M.;				
RT "Frz-1 is a secreted antagonist of Wnt signaling expressed in the Spemann organizer"; Cell 88:747-756 (1997).				
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.				
RN [3]				
RP SEQUENCE FROM N.A.				
RA Deutermann R., Wedlich D., Risau W.; Lottspeich F., Deutscher P., Boumester T., Kim S.H., Piccolo S., De Robertis E.M.;				
RT "Frz-1 is a secreted antagonist of Wnt signaling expressed in the Spemann organizer"; Cell 88:747-756 (1997).				
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.				
RN [3]				
RP SEQUENCE FROM N.A.				
RA Leyns L., Boumester T., Kim S.H., Piccolo S., De Robertis E.M.; Rattner A., Hsieh J.C., Smallwood P.M., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;				
RA "A family of secreted proteins contains homology to the cysteine-rich ligand-binding domain of frizzled receptors"; Proc. Natl. Acad. Sci. U.S.A. 94:2859-2863 (1997).				
RL [4]				
RP MEDLINE=7250455; PubMed=9096311;				
RA Rattner A., Hsieh J.C., Smallwood P.M., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;				
RA "A family of secreted proteins contains homology to the cysteine-rich ligand-binding domain of frizzled receptors"; Proc. Natl. Acad. Sci. U.S.A. 94:2859-2863 (1997).				
RL [4]				
RP SEQUENCE FROM N.A.				
RA Leyns L., Boumester T., Kim S.H., Piccolo S., De Robertis E.M.; Rattner A., Hsieh J.C., Smallwood P.M., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;				
RA "Frz-1 is a secreted antagonist of Wnt signaling expressed in the Spemann organizer"; Cell 88:747-756 (1997).				
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.				
RN [3]				
RP SEQUENCE FROM N.A.				
RA Leyns L., Boumester T., Kim S.H., Piccolo S., De Robertis E.M.; Rattner A., Hsieh J.C., Smallwood P.M., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;				
RA "Frz-1 is a secreted antagonist of Wnt signaling expressed in the Spemann organizer"; Cell 88:747-756 (1997).				
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.				
RN [3]				
RP SEQUENCE FROM N.A.				
RA Leyns L., Boumester T., Kim S.H., Piccolo S., De Robertis E.M.; Rattner A., Hsieh J.C., Smallwood P.M., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;				
RA "Frz-1 is a secreted antagonist of Wnt signaling expressed in the Spemann organizer"; Cell 88:747-756 (1997).				
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.				
RN [3]				
RP SEQUENCE FROM N.A.				
RA Leyns L., Boumester T., Kim S.H., Piccolo S., De Robertis E.M.; Rattner A., Hsieh J.C., Smallwood P.M., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;				
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RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.				
RN [3]				
RP SEQUENCE FROM N.A.				
RA Leyns L., Boumester T., Kim S				

Db 134 LACDELPPYDRGVCISPEANIVTAGDFPMDS-----TGHCRGASSERC 178
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 DR EMBL: U24163; AAC50736; 1;
 DR EMBL: U91903; AAB51298; 1;
 DR EMBL: U68057; AAC51217; 1;
 DR Genew: HGNC:3959; FRZB;
 DR MINI: 605083; 1;
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF01392; Fz; 1;
 DR Pfam: PF01759; NTR; 1;
 DR SMART: SMO0063; FRI; 1;
 DR PROSITE: PS50038; FZ; 1;
 DR Glycoprotein; Signal; 1;
 KW POTENTIAL.
 FT Glycoprotein; Signal; 1; 32
 FT FRIZZLED-RELATED PROTEIN.
 FT SIGNAL; 325
 FT CHAIN; 33 325
 FT FRIZZLED-RELATED PROTEIN.
 FT DOMAIN; 33 325
 FT DOMAIN; 165 294
 FT DOMAIN; 165 294
 FT SITE; 301 318
 FT SER-RICH.
 FT CARBOHYD 49 49
 FT CONFLICT 63 63
 FT CONFLICT 106 106
 SQ SEQUENCE 325 AA; 36254 MW; 8337C51BBA9A8B07 CRC64;
 Query Match 44.18; Score 828; DB 1; Length 325;
 Best Local Similarity 50.8%; Pred. No. 5.4e-62;
 Matches 164; Conservative 51; Mismatches 78; Indels 30; Gaps 8;

RESULT 3
 FRZB_HUMAN
 ID FRZB_HUMAN STANDARD: PRT; 325 AA.
 AC Q92265; Q00181; Q99686;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE FRizzled-related protein precursor (FrzB-1) (Frizzled) (Fritz).
 GN FRZB OR FRZB1 OR FRE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1] NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=96421609; PubMed=8824257;
 RA Hoang B., Moos M. Jr., Vukicevic S., Iuyten F.P.;
 RT "Primary structure and tissue distribution of FRZB, a novel protein
 related to Drosophila frizzled, suggest a role in skeletal
 morphogenesis";
 RT RL J. Biol. Chem. 271:26131-26137(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Mayr T., Deutsch U., Kuehl M., Drexlner H.C.A., Lottspeich F.,
 RA Deuzermann R., Wedlich D., Risau W.;
 RT "Frizz: a secreted frizzled-related protein that inhibits Wnt
 activity";
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=97236495; PubMed=9118218;
 RA Leyns L., Bouwmeester T., Kim S.-H., Piccolo S., de Robertis E.M.;
 RT "Frz-1 is a secreted antagonist of Wnt signaling expressed in the
 Spemann organizer";
 RT Cell 88:747-756(1997).
 RL FUNCTION: MAY BE INVOLVED IN MORPHOGENESIS OF SKELTON. MAY ALSO
 CC ACT AS A SOLUBLE WNT-BINDING PROTEIN THAT MAY ANTAGONIZE WNT
 CC SIGNALING.
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CARTILAGENOUS CORES
 CC OF THE LONG BONE DURING EMBRYONIC AND FETAL DEVELOPMENT AND IN THE
 CC APPENDICULAR SKELETON (6-13 WEEKS). AT 13 WEEKS OF GESTATION,
 CC TRANSCRIPTS WERE PRESENT IN EARLY CHONDROBLASTS OF THE TARSAL
 CC BONES OF THE FOOT, THE CARPAL BONES OF THE HANDS AND THE EPIPHYSIS
 CC OF LONG BONES. HIGHLY EXPRESSED IN PLACENTA AND HEART, FOLLOWED BY
 CC BRAIN, SKELETAL MUSCLE, KIDNEY AND PANCREAS. WEAKLY EXPRESSED IN
 CC LUNG AND LIVER.
 CC -!- DOMAIN: The Fz domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 NTR DOMAIN.

RESULT 4
 FZD5_HUMAN
 ID FZD5_HUMAN STANDARD:
 AC Q13467;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frizzled 5 precursor (Frizzled-5) (Fz5) (hFz5).
 GN FZD5 OR Fz5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates;
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=96224032; PubMed=8626600;

RA	Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.; "A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled.";	POTENTIAL, FRIZZLED 5, EXTRACELLULAR (POTENTIAL).
RT	J. Biol. Chem. 271:4468-4476(1996).;	1 (POTENTIAL).
RL	[2]	CYTOSMIC (POTENTIAL).
RN	SEQUENCE FROM N.A.	2 (POTENTIAL).
RX	MEDLINE#21301556; PubMed#11408929;	3 (POTENTIAL).
RA	Saitoh T., Hirai M., Katoch M.; "Molecular cloning and characterization of human Frizzled-5 gene on chromosome 2q33.3-q34 region"; Int. J. Oncol. 19:105-110(2001).;	CYTOSMIC (POTENTIAL).
RN	[3]	CYTOSMIC (POTENTIAL).
RP	SEQUENCE OF 273-331 FROM N.A.	4 (POTENTIAL).
RC	TISSUE=Oesophageal carcinoma;	CYTOSMIC (POTENTIAL).
RX	MEDLINE#98374323; PubMed#9707618;	EXTRACELLULAR (POTENTIAL).
RA	Tanaka S., Akiyoshi T., Mori M., Wands J.R., Sugimachi K.; "A novel frizzled gene identified in human esophageal carcinoma mediates APC/beta-catenin signals"; Proc. Natl. Acad. Sci. U.S.A. 95:10164-10169(1998).;	CYTOSMIC (POTENTIAL).
RL	[4]	CYTOSMIC (POTENTIAL).
RN	RP COUPLING TO BETA-CATENIN PATHWAY.	N-LINKED (GLCNAC. . .) (POTENTIAL).
RX	MEDLINE#97207341; PubMed#9054360;	7 (POTENTIAL).
RA	He X., Saint-Jeannet J.P., Wang Y., Nathans J., David I., Varmus H.; "A member of the Frizzled protein family mediating axis induction by Wnt-5A"; Science 275:1652-1654(1997).	7 (POTENTIAL).
RT	"-1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signalling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signalling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarized information during tissue morphogenesis and/or in differentiated tissues. Interacts specifically with Wnt5A to induce the beta-catenin pathway.	7 (POTENTIAL).
CC	"-1- SUBCELLULAR LOCATION: Integral membrane protein.	7 (POTENTIAL).
CC	"-1- DOMAIN: Lys-Thr-X-X-Tro motif is involved in the activation of the Wnt/beta-catenin signalling pathway (By similarity).	7 (POTENTIAL).
CC	"-1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).	7 (POTENTIAL).
CC	"-1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.	7 (POTENTIAL).
CC	"-1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.	7 (POTENTIAL).
CC	-----	-----
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DR	EMBL: U43318; AAC50385.1; "	RESULT 5
DR	EMBL: AB043702; BAB0939.1; "	FZD5_MOUSE STANDARD; PRT: 577 AA.
GENE	HGNC:043; FZDS.	AC Q9E0D0; 008975;
MMI	601723; "	CC 15-JUN-2002 (Rel. 41, Created)
DR	InterPro: IPR00539; Frizzled.	DT 15-JUN-2002 (Rel. 41, Last sequence update)
DR	InterPro: IPR00024; Fz-domain.	DT 15-JUN-2002 (Rel. 41, Last annotation update)
DR	InterPro: IPR00832; GPCR_Secretin.	DE Frizzled 5 precursor (Frizzled-5) (Fz-5) (mFz5).
DR	Pfam: PF01392; Fz_1.	GN FZ5.
DR	Pfam: PF1534; Frizzled.	OS Mus musculus (Mouse).
PRINTS	PRINTS: PR00489; FRIZZLED.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Rodentia; Sciurognath; Murinae; Mus.
SMART	SMART: SM00063; FRI_1.	NCBI_TaxID=10090;
PROSITE	PROSITE: PS50038; FZ_1.	RN [1]
PROSITE	PROSITE: PS50261; G-PROTEIN RECEPTOR_F2_4; 1.	RP SEQUENCE FROM N.A.
DR	Multigene family; G-protein coupled receptor; Transmembrane; Developmental protein; Glycoprotein; Signal.	RC STRAIN=C57BL/6N; TISSUE=Gut;
KW	"Mouse Wnt receptor gene Fzd5 is essential for yolk sac and placental angiogenesis";	RX Published=11092808;
DR	"Mouse Wnt receptor gene Fzd5 is essential for yolk sac and placental	RA Tsuchikawa T., Tamai Y., Zorn A.M., Yoshida H., Seldin M.F., Nishikawa S.-I., Taketo M.M.;
DR	Development 128:25-33(2001).	RT
RN	[2]	RL

RP	SEQUENCE OF 207-296 FROM N.A.	FT	TRANSMEM	399	419	5 (POTENTIAL).
RC	TISSUE=57BL/6; TISSUE=Prostate;	FT	DOMAIN	420	445	CYTOSPLASMIC (POTENTIAL).
RA	Johnson M.A., Greenberg N.M.	FT	TRANSMEM	446	466	(POTENTIAL).
RL	Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.	FT	DOMAIN	467	495	EXTRACELLULAR (POTENTIAL).
RN	[3]	FT	TRANSMEM	496	516	7 (POTENTIAL).
RP	TISSUE SPECIFICITY.	FT	DOMAIN	517	577	CYTOSPLASMIC (POTENTIAL).
RX	MEDLINE=96224032; PubMed=8626800;	FT	DOMAIN	28	150	PDZ - BINDING.
RA	Wang Y., Macke J.P., Abelina B.S., Andreasson K., Worley P.,	FT	CARBOHYD SITE	575	47	N-LINKED (GLCNAC, . . .) (POTENTIAL).
RA	Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;	FT	CARBOHYD	151	151	N-LINKED (GLCNAC, . . .) (POTENTIAL).
RT	"A large family of putative transmembrane receptors homologous to the product of the Drosophila tissue polarity gene frizzled.";	FT	SEQUENCE	577 AA;	63794 MW;	F6877c9b535C8B65 CRC64;
RL	J. Biol. Chem. 271:4468-4476(1996).					
-i-	FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in CC transduction and intercellular communication of polarity information during tissue morphogenesis and/or in differentiated tissues. Plays a role in yolk sac angiogenesis and in placental vascularization. Binds to Wnt2, Wnt5A, but not to Wnt2B or Wnt4.					
CC	-i- SUBCELLULAR LOCATION: Integral membrane protein.					
CC	-i- TISSUE SPECIFICITY: Expressed in eye, kidney, lung, chondrocytes, epithelial cells of the small intestine and goblet cells of the colon.					
CC	-i- DEVELOPMENTAL STAGE: Expressed in the yolk sac, placenta, eye and lung bud at 9.5 days post coitum (dpc). At 10.5 dpc, also expressed in the placental blood vessel of embryonic origin.					
CC	-i- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).					
CC	-i- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.					
CC	-i- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.					
CC	-----					
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CC	-----					
DR	AAC72146; AAC39355.1; -.					
DR	AF05203; AAC01933.1; -.					
DR	MGD:MGI:108511; P2d5.					
DR	InterPro: IPR000539; Frizzled.					
DR	InterPro: IPR000024; Fz-domain.					
DR	InterPro: IPR000834; GPR-secretin.					
DR	Pfam: PF01392; Fz_1.					
DR	PRINTS: PRO0049; FRIZZLED.					
DR	SMART: SM00063; FRI_1.					
DR	PROSITE: PS50038; Fz_1.					
DR	PROSITE: PS50061; G-PROTEIN_RECEP_F2_4; 1.					
KW	Multigene family; G-protein coupled receptor; transmembrane; Developmental protein; Glycoprotein; Signal.					
FT	SIGNAL	1	26			POTENTIAL.
FT	DOMAIN	27	577			FRIZZLED 5.
FT	TRANSMEM	27	234			EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	235	255	1		(POTENTIAL).
FT	TRANSMEM	256	266	2		CYTOSPLASMIC (POTENTIAL).
FT	TRANSMEM	267	287	2		(POTENTIAL).
FT	DOMAIN	288	311	3		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	312	332	3		(POTENTIAL).
FT	TRANSMEM	333	354	4		CYTOSPLASMIC (POTENTIAL).
FT	TRANSMEM	355	375	4		(POTENTIAL).
FT	DOMAIN	376	398	5		EXTRACELLULAR (POTENTIAL).

Houston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulip D., Lai Z., Lasko P., Lei Y., Levitt A.P., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkouloff G., Milashina N.V., Morris J., Mosherelli A., Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purif V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klaimos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Svartvold R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zweiziger J.S.-C., Zhan M., Zhang G., Zhao O., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.Q., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of *Drosophila melanogaster*"; *Science* 287:2185-2195 (2000).

-1- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of Gsk-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of Gsk-3 kinase. Both pathways seem to involve interactions with G-proteins. Required to coordinate the cioskeletal hairs and bristles.

-1- DEVELOPMENTAL STAGE: Expression starts at stage 6 in all cells between 15 and 70 per cent of egg length, including the invaginating cells of the ventral furrow. Stripe pattern is emerging by early stage 8. From stage 9 and continuing throughout embryogenesis, expression is seen in the developing CNS. At stage 10, expressed in 15 stripes in the presumptive head and trunk regions, in the posterior midgut primordium, in a subset of cells of anterior midgut invagination and in the procephalic lobe. At stage 12, expression declines in epidermis and increases in the midgut and visceral mesoderm. At stage 17, only expressed in the CNS, hindgut and dorsal vessel.

-1- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).

-1- DOMAIN: The fz domain is involved in binding with Wnt ligands.

-1- SIMILARITY: BELONGS TO FAMILY FZ/SHO OF G-PROTEIN COUPLED RECEPTORS.

-1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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EMBL: U65589; AAC47273.1; -
EMBL: AE00518; AAF19184.1; -
FlyBase: FBgn0016792; fz2.
InterPro: IPR000539; Frizzled.
InterPro: IPR00024; Fz-Domain.
InterPro: IPR00832; GPCR_secretrin.
PFAM: PF01534; Frizzled_1.
Pfam: PF01392; Fz_1.
PRINTS: PRO0489; FRIZ1.
SMART: SM00063; FRIZ1.
PROSITE: PS50261; G-PROTEIN_RECEP_F2_4; 1.
Multigene Family: Receptor_G-protein_coupled receptor; Transmembrane_Devopmental protein; Glycoprotein; Signal.

RT	mediates APC/beta-catenin signals.".	SQ	SEQUENCE	591 AA;	64466 MW;	0D3784A78DF0B2E5 CRC64;
RL	Proc. Natl. Acad. Sci. U.S.A. 95:1064-10169 (1998).		Query Match	16 6%;	Score 312;	DB 1;
CC	- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signalling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues.		Best Local Similarity	40.4%;	Pred. No. 1.4e-18;	Gaps 4;
CC	- TISSUE SPECIFICITY: Integral membrane protein. Localizes in the plasma membrane (By similarity).		Matches	63;	Conservative	27; Mismatches 46;
CC	- TISSUE LOCATION: Integral membrane protein. Localizes in the brain, testis, eye, skeletal muscle and kidney. Moderately expressed in pancreas, thyroid, adrenal cortex, small intestine and stomach. Detected in fetal liver and kidney.		QY	8 ALCLWHLALG-----VRG---APCEAVRIPMCRRMPNNTMRPMLHHSQEEN 53		
CC	- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).		DB	9 ALLLRLLAAGAALEIGRFPERGRGAAPQAEVPMCRGQVAPQAEVPMCRGQVAPQEGTSGQE 68		
CC	- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).		QY	54 AILAIQOEEELVDYNSAVLREFFCAYAPICTLEFLPKCKSVQRARDDEPLMK 113		
CC	- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.		DB	69 AAAELAEFAPLVQGGSHLRFFLCSLYAPCT-DQVSTPIPACRMCEQARLRCAPIME 127		
CC	- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.		QY	114 MYNHSPESLACDPELPYDGYCISPEAIVTDLPED 149		
CC	- CAUTION: Has been first described as FZD3 in literature.		Db	128 QFNFGWPDSLQCARLPTRN---DPHALCMEAOPEN 158		
CC	-----					
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CC	-----					
DR	DR: u82169; ARG51174.1; -.					
DR	MIM: 601766; -.					
DR	InterPro: IPR000539; Frizzled.					
DR	InterPro: IPR000024; Fz-domain.					
DR	InterPro: IPR000832; GPCR_secretin.					
DR	PFAM: PF01392; Fz_1.					
DR	PRINTS: PRO00489; FRIZZLED.					
DR	SMART: SM00063; FRI_1.					
DR	PROSITE: PS50038; FZ_1.					
DR	PROSITE: PS00261; G_PROTEIN_RECEP_F2_4; 1.					
KW	Multigene family; G-protein coupled receptor; Transmembrane; Developmental Protein; Glycoprotein; Signal.					
FT	SIGNAL 1 22 POTENTIAL.					
FT	CHAIN 23 591 229 FRIZZLED 9.					
FT	DOMAIN 23 250 1 (POTENTIAL).					
FT	TRANSMEM 230 266 CTOPLASMIC (POTENTIAL).					
FT	DOMAIN 251 267 287 2 (POTENTIAL).					
FT	TRANSMEM 267 315 EXTRACELLULAR (POTENTIAL).					
FT	DOMAIN 288 336 3 (POTENTIAL).					
FT	TRANSMEM 316 337 355 CYTOPLASMIC (POTENTIAL).					
FT	DOMAIN 337 356 376 4 (POTENTIAL).					
FT	TRANSMEM 356 377 400 EXTRACELLULAR (POTENTIAL).					
FT	DOMAIN 377 401 421 5 (POTENTIAL).					
FT	TRANSMEM 400 422 447 CYTOPLASMIC (POTENTIAL).					
FT	TRANSMEM 448 468 6 (POTENTIAL).					
FT	DOMAIN 469 508 EXTRACELLULAR (POTENTIAL).					
FT	TRANSMEM 509 529 7 (POTENTIAL).					
FT	DOMAIN 530 591 CTOPLASMIC (POTENTIAL).					
FT	TRANSMEM 534 555 FZ_2.					
FT	SITE 532 537 LYS-THR-X-X-TRP MOTIF.					
FT	CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).					
FT	CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).					
RESULT 8						
FZD9_MOUSE	STANDARD;					
ID	FZD9_MOUSE					
AC	Q9CX16; Q35434; Q9R2B3;					
DT	15-JUN-2002 (Rel. 41. Created)					
DT	15-JUN-2002 (Rel. 41. Last sequence update)					
DT	15-JUN-2002 (Rel. 41. Last annotation update)					
DE	Frizzled 9 Precursor (Frizzled 9) (Fz-9) (mFz9).					
GN	FZD9 OR FZD3.					
OS	Mus musculus (Mouse)					
OC	Bukarvita; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Murinae; Mus.					
OC	NCBI_TaxID:10090;					
RN	[1]					
RP	SEQUENCE FROM N.A. AND DEVELOPMENTAL STAGE.					
RC	STRAIN=C57BL/6J; TISSUE=Brain;					
RX	MEDLINE=99216417; Pubmed=10198163;					
RA	Wang Y-K.; Spoerle R.; Paperna T.; Schuchhart K.; Francke U.; Sciurognath; Muridae; Murinae; Mus.					
RT	"Characterization and expression pattern of the frizzled gene Fz9 in Williams-Beuren syndrome."					
RT	the mouse homolog of FZD9 which is deleted in Williams-Beuren syndrome."					
RL	Genomics 57: 235-248(1999).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=C57BL/6J; TISSUE=Embryonic head;					
RX	Medline=21085660; Pubmed=1121751;					
RA	Kawai J.; Shinagawa A.; Shibata K.; Itoh M.; Ishii Y.; Arakawa T.; Hara A.; Fukunishi Y.; Konno H.; Adachi J.; Fukuda S.; Aizawa K.; Izawa M.; Nishi K.; Kiyosawa H.; Kondo S.; Yamana I.; Saito T.; Okazaki Y.; Gojobori T.; Bono H.; Kasukawa T.; Saito R.; Kadota K.; Matsuda H.A.; Ashburner M.; Batalov S.; Fleischmann W.; Gaasterland T.; Gissi C.; King B.; Kochiwa H.; Riehl P.; Lewis S.; Matsuo Y.; Nikaido I.; Pesole G.; Quackenbush J.; Schriml L.M.; Steabili F.; Suzuki R.; Tomita M.; Wagner L.; Washio T.; Sakai K.; Okido T.; Furuno M.; Aono H.; Baldarelli R.; Barsh G.; Blake J.; Boffelli D.; Bojunga N.; Carninci P.; de Bonaldo M.F.; Brownstein M.J.; Bult C.; Fletcher C.; Fujita M.; Gariboldi M.; Gustincich S.; Hill D.; Holman M.; Hume D.A.; Kamaya M.; Lee N.H.; Nordone P.; Ring B.; Ringwald M.; Rodriguez I.; Safran M.; Sasaki H.; Sato K.; Schoenbach C.; Seya T.; Shihata Y.; Storch K.-P.; Suzuki H.; Toyo-oka K.; Wang K. H.; Whittaker C.; Wilming L.; Wynshaw-Boris A.; Yoshida K.; Hasegawa Y.; Kawaji H.; Kohtsuki S.; Hayashizaki Y.; Hayashizaki Y.;					
RT	"Functional annotation of a full-length mouse cDNA collection."					
RL	Nature 409: 685-690(2001).					
RN	[3]					
RP	SEQUENCE OF 44-592 FROM N.A.					
RA	Van Raay T.J.; Rasmussen J.T.; Rao M.S.;					
RT	"A novel mouse frizzled gene expressed in early neural development."					
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.					
RN	[4]					
RP	SEQUENCE OF 144-592 FROM N.A.					
RC	STRAIN=BALB/C;					

RA Calo L., Mimmack M.L., Keverne E.B., Emson P.C.;
"Localization of the mouse frizzled gene *mpZD3* in the olfactory epithelium and in the vomeronasal organ.";
RT Submitted (TJUL-1998) to the EMBL/GenBank/DDBJ databases.
RL -!- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors which are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signalling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Localizes in the plasma membrane.
CC -!- TISSUE SPECIFICITY: In the embryo, found in the neural tube, trunk skeletal muscle precursors (myotomes), limb skeletal anlagen, craniofacial regions and nephric ducts. In the adult, expression is abundant in heart, brain, testis and skeletal muscle. In the testis, expressed in all spermatogenic cell types. Lower levels in adult lung, liver and kidney. Barely detectable in spleen. Expressed also in chondrocytes.
CC -!- DEVELOPMENTAL STAGE: Not detected at embryonic day 7 (E7), weekly at E11 and strongly at E15 and E17. Expression covers the entire neural tube at day 9.5 post-coitum (dpc), decreases at 10.5 dpc and becomes detectable only in the lumbar to tail regions at 11.5 dpc. In the somites, expression begins at 10.5 dpc to become upregulated all along the rostrocaudal trunk axis at 11.5 dpc. In craniofacial territories, expression is first detected at 11.5 dpc in restricted areas of the nose, dorsally to the eye and second branchial arch anlagen. At 11.5 dpc, predominantly expressed in restricted areas of the nose, dorsally to the eye and in the caudal pharyngeal region.
CC -!- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).
CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).
CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
CC -!- CAUTION: Has been first described as FZ3 in literature.
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CC DR AF088850; AAD27789.1; -.
DR EMBL; AK021164; BAB3231.1; -.
DR EMBL; AF033385; AAB87503.2; -.
DR MGN; MG1:1313278; Fzdg.
DR InterPro; IPR000339; Frizzled.
DR InterPro; IPR000044; Fz_domain.
DR InterPro; IPR000332; GPCR_Secretin.
DR Pfam; PF01392; Fz_2.
DR Pfam; PF01534; Frizzled; 3.
DR PRINTS; PR00489; "FRIZZLED."
DR SMART; SM00063; FKL_1.
DR PROSITE; PS5003B; FZ_1.
DR PROSITE; PS50261; G-PROTEIN RECEPTOR_F2_4; 1.
KW Multigene family; G-protein coupled receptor; Transmembrane; Developmental Protein; Glycoprotein Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 592 FRIZZLED_9.
DOMAIN 24 230 EXTRACELLULAR.

RA TRANSMEM 231 1 (POTENTIAL).
TRANSMEM DOMAIN 252 CRYPTOPLASMIC (POTENTIAL).
TRANSMEM DOMAIN 252 2 (POTENTIAL).
TRANSMEM DOMAIN 289 288 EXTRACELLULAR (POTENTIAL).
TRANSMEM DOMAIN 316 316 3 (POTENTIAL).
TRANSMEM DOMAIN 338 356 CRYPTOPLASMIC (POTENTIAL).
TRANSMEM DOMAIN 357 377 4 (POTENTIAL).
TRANSMEM DOMAIN 378 401 EXTRACELLULAR (POTENTIAL).
TRANSMEM DOMAIN 402 422 5 (POTENTIAL).
TRANSMEM DOMAIN 423 448 CRYPTOPLASMIC (POTENTIAL).
TRANSMEM DOMAIN 449 469 6 (POTENTIAL).
TRANSMEM DOMAIN 470 509 EXTRACELLULAR (POTENTIAL).
TRANSMEM DOMAIN 510 530 7 (POTENTIAL).
TRANSMEM DOMAIN 531 592 CRYPTOPLASMIC (POTENTIAL).
TRANSMEM DOMAIN 35 156 FZ.
TRANSMEM SITE 533 538 LYS-THR-X-X-X-TRP MOTIF.
TRANSMEM CARBOHYD 54 54 N-LINKED (GLCNAC . .) (POTENTIAL).
TRANSMEM CONFLICT 66 66 N-LINKED (GLCNAC . .) (POTENTIAL).
TRANSMEM CONFLICT 73 74 S->P (IN REF 3).
TRANSMEM CONFLICT 93 93 QL->HC (IN REF 2).
TRANSMEM CONFLICT 144 144 L->F (IN REF 2).
TRANSMEM CONFLICT 221 221 P->S (IN REF 4).
TRANSMEM CONFLICT 237 237 A->P (IN REF 4).
TRANSMEM CONFLICT 308 308 D->G (IN REF 3).
TRANSMEM CONFLICT 374 374 V->F (IN REF 4).
TRANSMEM CONFLICT 592 592 L->P (IN REF 2).
SEQUENCE 592 AA; 64994 MW; 21B2D4F8CE32965 CRC64;

Query Match 16.5%; Score 310; DB 1; Length 592;
Best Local Similarity 39.7%; Pred. No. 2, 1-e-18;
Matches 62; Conservative 28; Mismatches 46; Indels 20; Gaps 4;

QY 8 ALCLWHLALG-----VRG--APCEAVRIPMCRIMPWNTRMPNLIHSTQEN 53
Db 10 ALLWLQLATGAELGRFDPERGPGAPCQAMEIPMCRIGYNUJTRMPNLGHTSQE 69

QY 54 ATLAIEQYEELVDVNCSAVLRFPCAMYAPICTLEFLHDPIKPKCSVCQRARDCEPLMK 113
Db 70 AAAQLAQAFSPLSVQYGCISHLREFLCSLYAPMCT-DQVSTP1PACRPMEQARLRCAPIME 128

QY 114 MYNHSPESLACDELPPYDRGYCISPAIAVTDLPD 149
Db 129 QFNFGWPDSLDCAIRLPTRN----DHALCMEPAN 159

RESULT 9

FAD7_XENLA STANDARD; PRT; 549 AA.
ID FAD7_XENLA STANDARD; PRT; 549 AA.
AC OPUK8; Q9W743; Q9W703; Q9IB13;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Frizzled 7 Precursor (Frizzled-) (FZ-7) (Xfz7).
GN FZ7.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Xenopodidae; Xenopus.
NCBI_TAXID=3355;
RN [1].
RN Sequence from N.A. MEDLINE=99376692; PubMed=10446283;
RX Wheeler G.N.; Hoppler S.;
RX RT "Two novel Xenopus frizzled genes expressed in developing heart and brain."
RT RL Mech. Dev. 86:203-207 (1999).
RN RN [2].
RN RP SEQUENCE FROM N.A., COUPLING TO BETA-CATENIN PATHWAY, AND PKC ACTIVATION.
RC TISSUE-Neurula;
RX MEDLINE=20133498; PubMed=10727861;
RA Medina A., Reintsch W., Steinbeisser H.;

-!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.	
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CC	EMBL; AP159106; ADD4331_1; -.
DR	EMBL; AP179213; ADD5267_1; -.
DR	EMBL; AJ243323; CAB45815_1; -.
DR	EMBL; AF114151; ADD21247_1; -.
DR	AF039215; AAF63152_1; -.
DR	InterPro; IPR000539; Frizzled.
DR	InterPro; IPR000034; Fz-domain.
DR	InterPro; IPR000832; GPC_R_secretin.
DR	PFam; PF01392; Fz_2.
DR	PFam; PF01534; Frizzled_2.
DR	PRINTS; SM00063; FRIZZLED.
DR	SMART; SM00063; FRI_1.
DR	PROSITE; PS50038; Fz_1.
DR	PROSITE; PS50261; G_protein_RECIP_F2_4_1.
KW	Multigene family; G-protein coupled receptor; Transmembrane;
KW	Developmental protein; Glycoprotein; Signal.
FT	SIGNAL_1
FT	CHAIN_2
FT	DOMAIN_23
FT	TRANSMEM_232
FT	DOMAIN_253
FT	TRANSMEM_263
FT	DOMAIN_264
FT	TRANSMEM_285
FT	DOMAIN_311
FT	TRANSMEM_312
FT	DOMAIN_333
FT	TRANSMEM_334
FT	TRANSMEM_355
FT	DOMAIN_376
FT	TRANSMEM_398
FT	DOMAIN_399
FT	TRANSMEM_419
FT	DOMAIN_420
FT	TRANSMEM_445
FT	DOMAIN_446
FT	TRANSMEM_467
FT	TRANSMEM_504
FT	DOMAIN_525
FT	TRANSMEM_524
FT	DOMAIN_549
FT	SITE_150
FT	SITE_527
FT	SITE_532
FT	SITE_547
FT	CARBODY_51
FT	CARBODY_51
FT	CARBODY_152
FT	CONFLICT_1
FT	CONFLICT_4
FT	CONFLICT_11
FT	CONFLICT_11
FT	CONFLICT_11
FT	CONFLICT_166
FT	CONFLICT_169
FT	CONFLICT_189
FT	CONFLICT_196
FT	CONFLICT_240
FT	CONFLICT_333
FT	CONFLICT_370
FT	CONFLICT_395
FT	CONFLICT_410
FT	CONFLICT_481
FT	CONFLICT_485
FT	CONFLICT_540
SO	SEQUENCE_549
AA	AA_62119 MW;
AA	DA44934BFF5949B CRC64;
Query Match	16.48;
Best Local Similarity	35.38;
Matches	27;
Conservative	27;
Pred. No.	2.5e-18;
Mismatches	70;
Indels	37;
gaps	8;

the mesoderm derivatives in the limb buds.

-1- DEVELOPMENTAL STAGE: First detected as stage 6 in the forming neural tube and somites, but not in trunk surface ectoderm. By stage 8, expression persists in the cranial ectoderm and is upregulated in the presumptive olfactory placodes. By stages 11-12, expression declines in the neural tube, but not in the cranial ectoderm; in somites, expressed all along the rostral-caudal axis as well as in presegmental mesenchyme caudal to the developing somites. Lens and otic placode expression first visible at stage 12, strongest at stages 13-16. Detected uniformly in ectoderm and mesenchyme of the limb primordia at stage 17. By stage 18, expression appears in the epibranchial placodes. By stages 22-30, highest levels in the most distal mesoderm of the autopod, in the ventricular zone of the neural tube from the forebrain to the spinal cord, in the dermomyotomes and the tail buds.

CC -1- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signalling pathway (By similarity).

CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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PRINTS: PR01534; PR01831; AAB87969; 1 . . . DR EMBL; AF224317; AAF61097; 1 . . . DR SMART; SM00653; FRI; 1 . . . DR InterPro; IPR00530; Frizzled. PROSTRE: PS50038; FZ; 1 . . . DR InterPro; IPR00024; Fz_domain. DR InterPro; IPR00083; GCR secretin. Pfam: PF01392; Fz; 1 . . . DR Pfam: PF01534; Frizzled; 1 . . . DR PRINTS: PR00489; FRIZZLED. SMART: SM00653; FRI; 1 . . . DR . . . PROSTRE: PS50261; G-PROTEIN_RECEP_F2_4; 1 . . . KW Multigene family; G-protein coupled receptor; Transmembrane; Developmental Protein; Glycoprotein; Signal.

POTENTIAL_1 31 FT SIGNAL 32 567 FT CHAIN 32 250 FT TRANSMEM 251 271 FT DOMAIN 272 282 FT TRANSMEM 283 303 FT DOMAIN 304 330 FT TRANSMEM 331 351 FT DOMAIN 352 373 FT TRANSMEM 374 394 FT DOMAIN 395 417 FT TRANSMEM 418 438 FT DOMAIN 439 464 FT TRANSMEM 465 485 FT DOMAIN 486 521 FT TRANSMEM 522 542 FT DOMAIN 543 567 FT DOMAIN 42 161 FT SITE 545 550 FT SITE 565 567 FT CARBOHYD 465 485 FT DOMAIN 486 521 FT TRANSMEM 522 542 FT DOMAIN 543 567 FT DOMAIN 42 161 FT SITE 545 550 FT SITE 565 567 FT CARBOHYD 61 61 FT DOMAIN 162 162 FT CONFICT 34 35 FT CONFICT 480 480 FT SEQUENCE 567 AA; 3E7F0381FC859BC3 CRC64;

POTENTIAL_2 31 FT CHAIN 32 567 FT TRANSMEM 250 271 FT DOMAIN 272 282 FT TRANSMEM 283 303 FT DOMAIN 304 330 FT TRANSMEM 331 351 FT DOMAIN 352 373 FT TRANSMEM 374 394 FT DOMAIN 395 417 FT TRANSMEM 418 438 FT DOMAIN 439 464 FT TRANSMEM 465 485 FT DOMAIN 486 521 FT TRANSMEM 522 542 FT DOMAIN 543 567 FT DOMAIN 42 161 FT SITE 545 550 FT SITE 565 567 FT CARBOHYD 61 61 FT DOMAIN 162 162 FT CONFICT 34 35 FT CONFICT 480 480 FT SEQUENCE 567 AA; 3E7F0381FC859BC3 CRC64;

POTENTIAL_3 31 FT CHAIN 32 567 FT TRANSMEM 250 271 FT DOMAIN 272 282 FT TRANSMEM 283 303 FT DOMAIN 304 330 FT TRANSMEM 331 351 FT DOMAIN 352 373 FT TRANSMEM 374 394 FT DOMAIN 395 417 FT TRANSMEM 418 438 FT DOMAIN 439 464 FT TRANSMEM 465 485 FT DOMAIN 486 521 FT TRANSMEM 522 542 FT DOMAIN 543 567 FT DOMAIN 42 161 FT SITE 545 550 FT SITE 565 567 FT CARBOHYD 61 61 FT DOMAIN 162 162 FT CONFICT 34 35 FT CONFICT 480 480 FT SEQUENCE 567 AA; 3E7F0381FC859BC3 CRC64;

Best Local Similarity 39.28; Pred. No. 4.2e-18; Matches 23; Mismatches 47; Indels 26; Gaps 5;

QY 12 WIHLA--LGVRGAPCEA-----VRIPMCRHMPNITRMPNHLHFST 50 CC -1- DOMAIN: LGVRGAPCEA-----VRIPMCRHMPNITRMPNHLHFST 50 Db 14 WIGLAAALLAALIGTPCAAAHHDEKAISVDPDHGFCOPSIPLTDIA NOTILPNLICHTN 73 CC -1- DOMAIN: WIGLAAALLAALIGTPCAAAHHDEKAISVDPDHGFCOPSIPLTDIA NOTILPNLICHTN 73 QY 51 QENAILATEQEELVDWYNCASAVLRFPIKAMYAPICTEFLADPIPKSVQRARDCEP 110 CC -1- DOMAIN: QENAILATEQEELVDWYNCASAVLRFPIKAMYAPICTEFLADPIPKSVQRARDCEP 110 Db 74 QEDAGLIEHQFYPLVKYQCSAELKFFLCSMYAPVCTV--LEGAIPORSILCERARQCEA 131 CC -1- DOMAIN: QEDAGLIEHQFYPLVKYQCSAELKFFLCSMYAPVCTV--LEGAIPORSILCERARQCEA 131 QY 111 LMKMYNHSWPESLACDELPLYDGRG-VCTISPEAVTVDLP 147 CC -1- DOMAIN: LMKMYNHSWPESLACDELPLYDGRG-VCTISPEAVTVDLP 147 Db 132 LMNKFGFWPERLURCNPVPHGAEICVGQN-TSDAP 167 CC -1- DOMAIN: LMNKFGFWPERLURCNPVPHGAEICVGQN-TSDAP 167

RESULT 13

FZDB_XENLA STANDARD; PRT; 581 AA.

ID FZDB_XENLA STANDARD; PRT; 581 AA.

AC 093274 ; QYI155;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Frizzled 8 precursor (Frizzled-8) (Fz-8) (xfzB).

GN FZB

OS Xenopus laevis (African clawed frog).

OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopoda; Xenopus.

OC NCB_1_TAXID=8355;

OX [1]

RN SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY.

RP TISSUE=Embryo;

RC TISSUE=Embryo;

RX PMID=3651509;

RX MEDLINE=98301424; PubMed=9636083;

RA Deardorff M.A.; Tan C.; Conrad L.J.; Klein P.S.;

RA Itoh K.; Jacob J.; Sokol S.Y.;

RT "A role for Xenopus Frizzled 8 in dorsal development.";

RT "Frizzled-8 is expressed in the Spemann organizer and plays a role in early morphogenesis.";

RL Mech. Dev. 74:145-157(1998).

RN [2]

RP SEQUENCE FROM N.A.

CC FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues. Activation by Wnt8, WntA or Wnt3A induces expression of beta-catenin target genes. Displays an axis-inducing activity.

CC SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- DEVELOPMENTAL STAGE: First expressed at high levels in the late blastula stages. At early gastrula, expressed in the deep cells of the Spemann organizer prior to involution of the dorsal blastopore lip. Detected in presumptive neuroectoderm as gastrulation proceeds. Becomes restricted to the anterior ectoderm by the end of gastrulation. At neurula stages, localized in the most anterior region of the embryo, mainly in the anterior ectoderm including telencephalic and cement gland regions.

CC -1- DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signalling pathway (By similarity).

CC -1- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

CC -1- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED

RECEPTORS	-!- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.	
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	DR EMBL; AF017177; AAC31121; 1.	Db 65 FWPLVIVHCSPLKFLCSMYPIC-LEDYKKPLPPCRSVBARACAPLMROYGFAWP 123
CC	DR EMBL; AF033110; AAC77361; 1.	Qy 121 ESLACDELPVYDRGCVISPEAVYDLPEDVKWIDTPDMYQERP---LDVDCRKRLSPD 176
CC	DR InterPro; IPR005329; Frizzled.	Db 124 DRMRCDRIP--EQG---NPDTLCMDP--NRTEQTTAASHPEPKPARSVPKGTRVEPP 178
CC	DR InterPro; IPR000832; GPCR_R_secretin.	Qy 177 R-----CKKKVKTPLATYLSKNSVYIHKAYORSGCNEVTVVVDKELFK 225
CC	DR Pfam; PF01392; Fz; 2.	Db 179 RSRSRATGCGESGCCQR--APMVQV-- SNERPLYNVRVTGQ----- 215
CC	DR Pfam; PF01534; Frizzled; 2.	Qy 226 SSSPPRPTQVPLTNSSQCQCPHLPHQDV-----IMCYENRSMMLLENCLVEKW 276
CC	DR SMART; SM00063; FRI; 1.	Db 216 -----IPNCAMP----CHNPFPSPEERTFTEWIGLMSVLCF--ASTPATVSTFLIDME 263
DR PROSITE; PS50038; Fz; 1.	RESULT 14	
DR KW Multigene family; G-protein coupled receptor; Transmembrane; developmental protein; Glycoprotein; Signal.	FZD1_CHICK STANDARD;	PRT; 592 AA.
KW SIGNAL	ID FZD1_CHICK_09IA07;	
FT 23	AC 057328; 09IA07;	
FT CHAIN 1	DT 15-JUN-2002 (Rel. 41, Created)	
FT DOMAIN 24	DT 15-JUN-2002 (Rel. 41, Last sequence update)	
FT DOMAIN 24	DT 15-JUN-2002 (Rel. 41, Last annotation update)	
FT TRANSMEM 240	DE Frizzled 1 precursor (Frizzled-1) (Fz-1) (cFz-1).	
FT DOMAIN 261	GN FZD1 OR FZ1.	
FT TRANSMEM 271	OS Gallus gallus (Chicken).	
FT DOMAIN 292	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
FT TRANSMEM 293	OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
FT DOMAIN 321	OC Gallulus.	
FT DOMAIN 342	OX NCBI_TaxID:9031;	
FT TRANSMEM 378	RN [1]	
FT DOMAIN 399	RP SEQUENCE FROM N.A.	
FT TRANSMEM 408	RC TISSUE="limb bud";	
FT DOMAIN 429	RX MEDLINE=98260739; PubMed=9598377;	
FT TRANSMEM 455	RA Kengaku M., Twombly V., Tabin C.C.	
FT DOMAIN 476	RT "Expression of wnt and frizzled genes during chick limb bud development.";	
FT TRANSMEM 506	RL Cold Spring Harb. Symp. Quant. Biol. 62:421-429(1997).	
FT DOMAIN 527	RN [2]	
FT DOMAIN 529	RP SEQUENCE OF 307-592 FROM N.A.	
FT SITE 579	RX MEDLINE=20245119; PubMed=10781956;	
FT CARBOHYD 42	RA Stark M.R., Biggs J.J., Schoenwolf G.C., Rao M.S.;	
FT CONFLICT 146	"Characterization of avian frizzled genes in cranial placode	
FT CONFLICT 1	RT development.";	
FT CONFLICT 3	RT	
FT CONFLICT 7	CC FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors, inhibition of	
FT CONFLICT 10	CC are coupled to the beta-catenin canonical signaling pathway, which	
FT CONFLICT 14	CC leads to the activation of dishevelled proteins, inhibition of	
FT CONFLICT 20	CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation	
FT CONFLICT 135	CC of wnt target genes. A second signalling pathway involving PKC and	
FT CONFLICT 171	CC calcium fluxes has been seen for some family members, but it is	
FT CONFLICT 175	CC not yet clear if it represents a distinct pathway or if it can be	
FT CONFLICT 185	CC integrated in the canonical pathway, as PKC seems to be required	
FT CONFLICT 216	CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem	
FT CONFLICT 237	CC to involve interactions with G-proteins. May be involved in	
FT CONFLICT 494	CC transduction and intercellular transmission of polarity	
FT CONFLICT 500	CC information during tissue morphogenesis and/or in differentiated	
FT CONFLICT 547	CC tissues.	
FT CONFLICT 565	-!- TISSUE SPECIFICITY: Integral membrane protein.	
FT CONFLICT 572	CC wall of the vesicle) and in epibranchial placode. Also expressed	
SQ SEQUENCE 581 AA:	CC in the developing somites (dermomyotome).	
Query Match 3 LSLVALCWLH -LALGWRCACEAVERIPCMCRHMPNNTTRPMNHHSQNEAIIAQ 60	CC in the developing somites (dermomyotome).	
Best Local Similarity 6 LSLLL-LYSWLGQSQAARKAKELSQCLTQVPLCKDIGNTYMPNQFNHDTOEAGMEVHQ 64	-!- DEVELOPMENTAL STAGE: Somites and placodal expression appears at	
Matches 61 YEELVDVNCASVLRFFCAMYAPCTLEFLHDPIKPCSKSVCORADCEPLMKMYNHSWP 120	CC stage 9. At this stage, more obvious expression is detected in the	
Qy 3 LSLVALCWLH -LALGWRCACEAVERIPCMCRHMPNNTTRPMNHHSQNEAIIAQ 60	CC neural tube (midbrain and rostral hindbrain), and persists through	
Db 6 LSLLL-LYSWLGQSQAARKAKELSQCLTQVPLCKDIGNTYMPNQFNHDTOEAGMEVHQ 64	CC about stage 15. Strongly expressed in the ectoderm and around the	
Qy 61 YEELVDVNCASVLRFFCAMYAPCTLEFLHDPIKPCSKSVCORADCEPLMKMYNHSWP 120	CC otic placodes at stage 12. At stage 16, otic expression declines,	
	CC Expression in epibranchial placodes begins and peaks at stage 20.	
	CC Expression in the lens of the eye is first seen at about stage 15.	

more evident at stage 16. At stage 17, seen in the ectoderm and mesenchyme of the limb primordia. Detected at stage 20 in the lip of the optic cup, in the mesenchyme surrounding the eye, in the ectoderm overlying the lens and in the ectoderm caudal and ventral of the olfactory placodes. From stages 20-30, expressed in cartilage and in the dermatomyotomes and migrating sclerotomal cells forming vertebrae.

-1 DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity).

-1 DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).

-1 SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.

-1 SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

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CC EMBL; AF031830; AAF87968; 1. ;
 CC DR InterPro; IPR00539; Fz_domain.
 CC DR InterPro; IPR00534; Frizzled.
 CC DR InterPro; IPR00024; Fz_domain.
 DR PROTE: PS50261; G-PROTEIN-RECEP_F2_4; 1.
 KW Multigene family; G-protein coupled receptor; Transmembrane;
 KW Developmental protein; Glycoprotein; Secretin; Signal.

FT SIGNAL 1 48
 FT -CHAIN 49 592
 FT DOMAIN 49 271
 FT TRANSEM 272 292
 FT DOMAIN 293 303
 FT TRANSEM 304 324
 FT DOMAIN 325 351
 FT TRANSEM 352 372
 FT DOMAIN 373 394
 FT TRANSEM 395 415
 FT DOMAIN 416 438
 FT TRANSEM 439 459
 FT DOMAIN 460 485
 FT TRANSEM 486 506
 FT DOMAIN 507 546
 FT TRANSEM 547 567
 FT DOMAIN 568 592
 FT DOMAIN 65 184
 FT SITE 570 575
 FT CARBOHYD 84 84
 FT CARBOHYD 185 185
 FT CARBOHYD 533 533
 SQ SEQUENCE 592 AA: 65490 MW: 933E7663CA6109D CRC64;

Query Match Score 305.5; DB: 1; Length 592;
 Best Local Similarity 42.9%; Pred.: No. 4.9e-18;
 Matches 57; Conservative 25; Mismatches 42; Indels 9; Gaps 3;

QY 16 ALGVGAP-----CEAVRIPMCRHMPNINTRMPNHLHHSTQENAILAEQYEELDVNC 69
 Db 56 ALSERGISTIPDHGVCQPISPLCTDIAYNOTIMPNLIGHTQEDAGLEHQFYPLVKVQC 115

Qy 70 SAVIRFEFAMYAPICTLEFLHPPIKEPKSVQRDCEPDKMVKHNSWPPBSLAQDLP 129
 Db 116 SAEUKFLCSMYAPVCTV-LEQALPPCRSLCERARQGCEALMNKGFGQWPDTLRCFKP 173

CC QY 130 VYDRG-VCTISPEA 141
 CC Db 174 VHSGAEIICVGQNA 186

RESULT 15
 FZDB_MOUSE STANDARD; PRT; 685 AA.
 ID FZDB_MOUSE
 AC Q61091
 DT 15-JUN-2002 (Rel. 41; Created)
 DT 15-JUN-2002 (Rel. 41; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Frizzled 8 precursor (Frizzled-8) (FZ-8) (mfz8).
 GN FZDB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 OC NCBL_TAXID=10090;
 OX [1]
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=96224032; PubMed=8626800;
 RA Wang Y.; Macke J.P.; Abella B.S.; Andreasson K.; Worley P.;
 RA Gilbert D.J.; Copeland N.G.; Jenkins N.A.; Nathans J.;
 RA Sheldahl L.C.; Park M.; Malbon C.C.; Moon R.T.;
 RT "Protein kinase C is differentially stimulated by Wnt and Frizzled
 product of the Drosophila tissue polarity gene frizzled.";
 RL J. Biol. Chem. 271:4468-4476(1996).
 RN [2]
 RP COUPLING TO BETA-CATENIN PATHWAY;
 RX MEDLINE=99324245; PubMed=10395542;
 RA Sheildahl L.C.; Park M.; Malbon C.C.; Moon R.T.;
 RT "Protein kinase C is differentially stimulated by Wnt and Frizzled
 homologs in a G-protein-dependent manner.";
 CC [-] FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signalling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues. Activation by Wnt8 induces expression of beta-catenin target genes.
 CC [-] SUBCELLULAR LOCATION: Integral membrane protein.
 CC [-] TISSUE SPECIFICITY: Expressed in chondrocytes.
 CC [-] DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wnt/beta-catenin signaling pathway (By similarity); the fz domain is involved in binding with Wnt ligands (By similarity).
 CC [-] DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).
 CC [-] SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.
 CC [-] SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; U43321; AAC52433.1; -.
 DR MG1; 108460; Fzd8.
 DR InterPro; IPR000539; Frizzled.
 DR IPR00024; Fz_domain.
 DR InterPro; IPR01392; Fz; 1.
 DR Pfam; PF01534; Frizzled; 1.
 DR PRINTS; PRO489; FRIZZLED.

DR SMART; SM00063; FRI; 1.
 DR PROSITE; PS3038; FZ; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Multigene family; G-protein coupled receptor; Transmembrane;
 developmental protein; Glycoprotein; Signal.

FT SIGNAL	1	27	POTENTIAL.
FT CHAIN	28	685	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	273	293	1 (POTENTIAL).
FT DOMAIN	294	309	CYTOSMERIC (POTENTIAL).
FT TRANSMEM	310	330	2 (POTENTIAL).
FT DOMAIN	331	394	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	395	415	3 (POTENTIAL).
FT DOMAIN	416	437	CYTOSMERIC (POTENTIAL).
FT TRANSMEM	438	458	4 (POTENTIAL).
FT DOMAIN	459	481	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	482	502	5 (POTENTIAL).
FT DOMAIN	503	530	CYTOSMERIC (POTENTIAL).
FT TRANSMEM	531	551	6 (POTENTIAL).
FT DOMAIN	552	582	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	583	603	7 (POTENTIAL).
FT DOMAIN	604	685	CYTOSMERIC (POTENTIAL).
FT DOMAIN	30	151	FZ.
FT DOMAIN	168	173	POLY-PRO.
FT DOMAIN	353	361	POLY-ALA.
FT DOMAIN	640	654	POLY-GLY.
FT SITE	606	611	LYS-THR-X-X-TRP MOTIF.
FT SITE	683	685	PDZ-BINDING.
FT CARBOHYD	49	49	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	152	152	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	473	473	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ • SEQUENCE	685	Aa;	73215 MW; P333B49474411267 CRC64;

Query Match 16.2%; Score 305; DB 1; Length 685;
 Best Local Similarity 39.5%; Pred. No. 6.4e-18;
 Matches 58; Conservative 31; Missmatches 46; Indels 12; Gaps 5;

Qy 4 SILVALCILWHLALGVRA----PCEAVRIPMCRRMPWNTTRMPNHLHSTQENAILAI 58
 Db 11 SLLAALAV-LQRSSGAAAASAKELACCEITVPLCKIGIYNTYMPHQFNHDTODEAGLEV 69

Qy 59 EOEVELVDVNCNSAVLRFCCAYAPICLTLEFLHDPIKPKCSVCQRARDDCBPLMKNYNHS 118
 Db 70 HQFWPLVNEIQCSPLKPFCLSMYTPIC-LEDYKKLPPCRSVCERAKAGCAPLMROYGFA 128

Qy 119 WPESLACDELPPYDRGYCISPAIVTD 145
 Db 129 WPDMMRCDRLP--EQG --NPDTLCMD 150

Search completed: March 7, 2003, 11:24:18

Job time : 16 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 7, 2003, 11:20:59 ; Search time 35 Seconds

(without alignments)
2036.923 Million cell updates/sec

Title: US-09-909-775-2

Perfect score: 1879

Sequence: MFLSILVALCLWLHLALGVR. SPKKNIKTRSAQKRTNPKRV 346

Scoring table: BL05UN62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:

671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_hexebrate:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_roron:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriapl:*

17: sp_archaeap:*

ALIGNMENTS

RESULT 1

014877

PRELIMINARY;

PRT; 346 AA.

ID 014877;

AC 014877;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE PTPHE.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TAXID=3606;

RN [1]

SEQUENCE FROM N.A.

RC TISSUE-ENDOMETRITUM;

RC Abu Jawdeh G.M., Comella N., Brown L.F., Tognazzi K., Kocher O.;

RT "frizzled protein frpHE (Homo Sapiens)"

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

DR AF026692; AAC04617.1; .

DR InterPro; IPR000024; Fz_domain.

DR InterPro; IPR001134; NetrIn_C.

DR PF01382; Fz; 1.

DR Pfam; PF01759; NTR; 1.

DR SMART; SM00063; FRI; 1.

DR PROSITE; PS50338; Fz; 1.

SQ SEQUENCE 346 AA; 39860 MW;

75D78D43E44CC2A CRC64;

DR Best Local Similarity 100.0%; Score 1879; DB 4; Length 346;

Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFLSILVALCLMLHALGVRGAPEAVRIPMCRMPWNITRPNHLHSTQENAILAEQ 60

Db 1 MFLSILVALCLMLHALGVRGAPEAVRIPMCRMPWNITRPNHLHSTQENAILAEQ 60

Qy 61 YEEELDVNCASAVLRFPCAMAPICTEFLIDPIKPKCSVORARDCEPILMKYHNSWP 120

Db 61 YEEELDVNCASAVLRFPCAMAPICTEFLIDPIKPKCSVORARDCEPILMKYHNSWP 120

0918v7 brachydanno

09y100 brachydano

09w6e5 brachydano

09ptt7 brachydano

090zt2 homo sapien

Q8AN2

090zt3 brachydano

098si2 brachydano

09y149 brachydano

09pwk6 brachydano

09pwk6 brachydano

09pwn8 brachydano

08qfmi3 brachydano

09y171 brachydano

096b74 homo sapien

09w6e2 brachydano

09u3z2 hydra atten

09u8u6 caenorhabdi

09pbn8 brachydano

09pnt3 brachydano

090yl7 brachydano

090wm3 brachydano

08tav8 homo sapien

09w6e2 brachydano

098u6 caenorhabdi

09pbt8 brachydano

09w6e3 brachydano

010662 caenorhabdi

09n532 caenorhabdi

000546 homo sapien

073821 xenopus lae

019116 bos taurus

008861 mus musculu

0918.5 17.0 577 13 0918v7

0918.5 17.0 579 13 09y100

0918.5 17.0 579 13 09w6e4

20 317.5 16.9 579 13 09ptt7

21 312 16.6 591 4 Q8AN2

22 303.5 16.2 559 13 090zt3

23 302.5 16.1 559 13 098si2

24 302 16.1 576 13 09y149

25 302 16.1 576 13 09pwk6

26 302 16.1 576 13 09pwn8

27 301.5 16.0 557 13 09pnt3

28 300.5 16.0 550 13 090yl7

29 298.5 15.9 574 4 Q9B74

30 291 15.5 592 13 09w6e2

31 283 15.1 568 5 01647

32 279 14.8 550 5 09BU6

33 268.5 14.3 580 13 09pbt8

34 261.5 14.3 580 13 09w6e3

35 268.5 14.3 580 13 090wm3

36 265 14.1 537 4 Q8PAV8

37 257.5 13.7 545 5 090322

38 248 13.2 295 13 01T897

39 247.5 13.2 920 5 Q9P13

40 237.5 12.6 525 5 010662

41 237.5 12.6 529 5 09n532

42 233 12.4 313 4 000546

43 232.5 12.4 281 13 073821

44 230 12.2 308 6 019116

45 230 12.2 314 11 008861

0918.5 17.0 577 13 0918v7

0918.5 17.0 579 13 09y100

0918.5 17.0 579 13 09w6e4

20 317.5 16.9 579 13 09ptt7

21 312 16.6 591 4 Q8AN2

22 303.5 16.2 559 13 090zt3

23 302.5 16.1 559 13 098si2

24 302 16.1 576 13 09y149

25 302 16.1 576 13 09pwk6

26 302 16.1 576 13 09pwn8

27 301.5 16.0 557 13 09pnt3

28 300.5 16.0 550 13 090yl7

29 298.5 15.9 574 4 Q9B74

30 291 15.5 592 13 09w6e2

31 283 15.1 568 5 01647

32 279 14.8 550 5 09BU6

33 268.5 14.3 580 13 09pbt8

34 261.5 14.3 580 13 09w6e3

35 268.5 14.3 580 13 090wm3

36 265 14.1 537 4 Q8PAV8

37 257.5 13.7 545 5 090322

38 248 13.2 295 13 01T897

39 247.5 13.2 920 5 Q9P13

40 237.5 12.6 525 5 010662

41 237.5 12.6 529 5 09n532

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43 232.5 12.4 281 13 073821

44 230 12.2 308 6 019116

45 230 12.2 314 11 008861

0918.5 17.0 577 13 0918v7

0918.5 17.0 579 13 09y100

0918.5 17.0 579 13 09w6e4

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30 291 15.5 592 13 09w6e2

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34 261.5 14.3 580 13 09w6e3

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36 265 14.1 537 4 Q8PAV8

37 257.5 13.7 545 5 090322

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43 232.5 12.4 281 13 073821

44 230 12.2 308 6 019116

45 230 12.2 314 11 008861

0918.5 17.0 577 13 0918v7

0918.5 17.0 579 13 09y100

0918.5 17.0 579 13 09w6e4

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31 283 15.1 568 5 01647

32 279 14.8 550 5 09BU6

33 268.5 14.3 580 13 09pbt8

34 261.5 14.3 580 13 09w6e3

35 268.5 14.3 580 13 090wm3

36 265 14.1 537 4 Q8PAV8

37 257.5 13.7 545 5 090322

38 248 13.2 295 13 01T897

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40 237.5 12.6 525 5 010662

41 237.5 12.6 529 5 09n532

42 233 12.4 313 4 000546

43 232.5 12.4 281 13 073821

44 230 12.2 308 6 019116

45 230 12.2 314 11 008861

0918.5 17.0 577 13 0918v7

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0918.5 17.0 579 13 09w6e4

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21 312 16.6 591 4 Q8AN2

22 303.5 16.2 559 13 090zt3

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27 301.5 16.0 557 13 09pnt3

28 300.5 16.0 550 13 090yl7

29 298.5 15.9 574 4 Q9B74

30 291 15.5 592 13 09w6e2

31 283 15.1 568 5 01647

32 279 14.8 550 5 09BU6

Qy	121	ESTACDELPHYDRGVCISPEAIVTVDLIEDPVKWDITPDMMVQERPLDVDCRKLSPDRCKC	180	Db	301	KKQIASRTSRTSRNSNPFSKGRPPAPKAPSPKKNIKARSAPKKSNLK	348
Db	121	ESTACDELPHYDRGVCISPEAIVTVDLIEDPVKWDITPDMMVQERPLDVDCRKLSPDRCKC	180		RESULT 3		
Qy	181	KKVPTLATYLSKNYSVTIHKAVQRSGCNEVTVVDKEIFKSSSPPIRTOVLITN	240		Q9JLS5	PRELIMINARY;	PRT;
Db	181	KKVPTLATYLSKNYSVTIHKAVQRSGCNEVTVVDKEIFKSSSPPIRTOVLITN	240		ID Q9JLS5	348 AA.	
Qy	241	SSQCOPHILPHODVLIMCYENRSRMMILENCLEVKWRDQLSKRSKSIWEERLQEQRRTVQD	300		AC Q9JLS5;		
Qy	241	SSQCOPHILPHODVLIMCYENRSRMMILENCLEVKWRDQLSKRSKSIWEERLQEQRRTVQD	300		DT 01-OCT-2000	(TREMBLrel. 15, Created)	
Db	241	SSQCOPHILPHODVLIMCYENRSRMMILENCLEVKWRDQLSKRSKSIWEERLQEQRRTVQD	300		DT 01-OCT-2000	(TREMBLrel. 15, Last sequence update)	
Qy	301	KKTAGRTSRSNPPKPKPAPKAPSKPKKNIKTRSAQKRNPKR	346		DE Frizzled related protein.		
Db	301	KKTAGRTSRSNPPKPKPAPKAPSKPKKNIKTRSAQKRNPKR	346		OS Rattus norvegicus (Rat).		
OS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			OC		
NCBI_TaxID		NCBI_TaxID=10116;			OX		
RN		[1]			RN		
RP		SEQUENCE FROM N.A.			RP		
RC		STRAIN=FISHER;			RC		
RX		PubMed=11485313;			RX		
RA		Wong V.K.W., Wong J.W.P., Chan J.W.P., Hsiao W.L.W.;			RA		
RT		"transcriptional activity of the promoter region of rat frizzled-			RT		
DT	01-MAY-1999	(TREMBLrel. 10, Created)			RT	related protein gene,"	
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)			RL	Biochem. Biophys. Res. Commun. 286:94-100(2001).	
DT	01-OCT-2001	(TREMBLrel. 18, Last annotation update)			DR	EMBL; AF140346; AAF66480.1; -;	
DE		Secreted frizzled-related sequence protein 4.			DR	InterPro; IPR000024; Fz-domain.	
GN		SFRP4.			DR	InterPro; IPR01134; Netrin_C.	
OS		Mus musculus (Mouse).			DR	PF0132; Fz; -;	
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			DR	PF01739; NTR; 1.	
NCBI_TaxID		NCBI_TaxID=10090;			DR	SMART; SM0063; FRI; 1.	
RN		[1]			DR	PROSITE; PS0038; FZ; 1.	
RP		SEQUENCE FROM N.A.			SQ	SEQUENCE 348 AA; 39718 MW; 6CA7979D5AC6A97 CRC64;	
RA		Chang J.T., Esumi N., Moore K., Li Y., Zhang S., Chew C., Goodman B., Rattner A., Moody S., Stettini G., Campochiaro P.A., Zack D.J.; RT "Cloning and characterization of a secreted frizzled-related protein that is expressed by the retinal pigment epithelium."			Query Match	92.4%; Score 1732; DB 11;	Length 348;
RT		that is expressed by the retinal pigment epithelium."			Best Local Similarity	92.5%; Pred. No. 1, 9e-10;	
RL		Hum. Mol. Genet. 0:0-019991;			Matches	8; Mismatches 18; Indels 0; Gaps 0;	
DR		DR			QY	1 MFLSILVALCLMLHALGVRGAPCEAVRIPMCRHMPPNITRMPNHLHSTQENALIEQ	60 *
DR		DR			DB	1 MLLSILVALCLMLURLAAGVRGAPCEAVRIPMCRHMPPNITRMPNHLHSTQENALIGQ	60
DR		InterPro; IPR000024; Fz-domain.			QY	61 YEELVDYNCSAVLRFIFCAMYAPICTLEFLHDPICKPSVQORARDCEPLMKMYNHSPW	120
DR		InterPro; IPR01134; Netrin_C.			DB	61 YEELVDYNCSVSLFFLCAMYAPICTLEFLHDPICKPSVQORARDCEPLMKMYNHSPW	120
Pfam		Pfam; PF01392; Fz; 1.			QY	121 ESLACDELPVYDGVCSPEALVTDLVEDVKWMDITPDMVQERPLDVDCRKLSPDRCKC	180
Pfam		SMART; SM01759; NTR; 1.			DB	121 ESLACDELPVYDGVCSPEALVTDLFEDVKWMDITPDMVQERSPFADCKHLSPLDRCKC	180
SMART		SMART; SM00063; FRI; 1.			QY	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
PROSITE		PROSITE; PS00038; FZ; 1.			DB	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
SEQ	SEQUENCE	351 AA; 40342 MW; 6CB0B25920A54FE CRC64;			QY	241 SSCQCOPHILPHODVLIMCYENRSRMMILENCLEVKWRDQLSKRSKSIWEERLQEQRRTVQD	300
Qy	1	MFLSILVALCLMLHALGVRGAPCEAVRIPMCRHMPPNITRMPNHLHSTQENALIEQ	60		DB	241 SSCQCOPHILPHODVLIMCYENRSRMMILENCLEVKWRDQLSKRSKSIWEERLQEQRRTVQD	300
Db	1	MERSILVALCLMLURLAAGVRGAPCEAVRIPMCRHMPPNITRMPNHLHSTQENALIEQ	60		QY	301 KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345
Qy	61	YEELVDYNCSAVLRFIFCAMYAPICTLEFLHDPICKPSVQORARDCEPLMKMYNHSPW	120		DB	301 KKQIASRTSRSNPPKPKGKPPKAPSPKKNIKTRSAQKRNPKR	345
Db	61	YEELVDYNCSVSLFFLCAMYAPICTLEFLHDPICKPSVQORARDCEPLMKMYNHSPW	120		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	121	ESTACDELPHYDRGVCISPEAIVTVDLIEDPVKWDITPDMMVQERPLDVDCRKLSPDRCKC	180		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	121	ESTACDELPHYDRGVCISPEAIVTVDLIEDPVKWDITPDMMVQERSFADCKHLSPLDRCKC	180		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	181	KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
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Qy	241	SSQCOPHILPHODVLIMCYENRSRMMILENCLEVKWRDQLSKRSKSIWEERLQEQRRTVQD	300		Db	241 SSCQCOPHILPHODVLIMCYENRSRMMILENCLEVKWRDQLSKRSKSIWEERLQEQRRTVQD	300
Db	241	SSQCOPHILPHODVLIMCYENRSRMMILENCLEVKWRDQLSKRSKSIWEERLQEQRRTVQD	300		Qy	301 KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	301 KKQIASRTSRSNPPKPKGKPPKAPSPKKNIKTRSAQKRNPKR	345
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
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Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
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Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
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Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
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Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
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Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
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Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
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Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Qy	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Qy	181 KKVKPTLATYLSKNYSVTIHKAVQRSGCNEVTTVVDKEIFKSSSPIPRTQVPLTN	240
Db	301	KKTAGRTSRSNPPKPKGKPPKAPKAPSPKKNIKTRSAQKRNPKR	345		Db		

RN	[1]	DR	Pfam; PF01759; NTR; 1..
RP	SEQUENCE FROM N.A.	DR	BROSITE; PS50038; Fz; 1..
RC	STRAIN=SPRAGUE-DAWLEY;	SQ	SEQUENCE 303 AA; 34507 MW; 8AB612A48933AAE1 CRC64;
RA	Wolf V., Artuso L., Dharmarajan A.; Guo K., Bielke W., Friis R.R.; Friis R.R.;	Query Match	79.0%; Score 1485; DB 11; Length 303;
RT	"Apoptosis-associated Gene Expression in Corpus luteum of the Rat.";	Best Local Similarity	96.1%; Pred. No. 6; e-128;
RL	A frizzled related gene is upregulated in Physiological Apoptosis."	Matches 273; Conservative	2; Mismatches 19; Indels 0; Gaps 0;
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY;	DR	MFLSILVALCLMHLALGVRGAPCEAVRIPCMCRHMWNITRMPNHLHSTQENALIAEQ 60
RA	Guo K., Wolf V., Dharmarajan A., Feng Z., Bielke W., Susanne S., Friis R.R.;	Db	MFLSILVALCLMHLALGVRGAPCEAVRIPCMCRHMWNITRMPNHLHSTQENALIAEQ 60
RT	"Apoptosis-associated Gene Expression in Corpus luteum of the Rat.";	DR	YEEELVDYNCASAVLRFPCAMYAPICTLEFLHDPIKECKSVICQARDDCEPLMKMYNHSWP 120
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.	Db	YEEELVDYNCASVLSFLCAMYAPICTLEFLHDPIKECKSVICQARDDCEPLMKMYNHSWP 120
DR	AF012891; AAB65431..1..	DR	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180
DR	InterPro; IPR00024; Fz_domain.	Db	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180
DR	InterPro; IPR01134; Netrin_C.	DR	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180
PFAM	PF01192; Fz; 1..	DR	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180
SMART	SM00063; FRI; 1..	DR	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180
PROSITE	PS50038; Fz; 1..	DR	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180
SQ	SEQUENCE 348 AA; 39735 MW; 08BA5BF909AE7B64 CRC64;	DR	KKVKPITLEATLSKNSYYVIHAKIKAYQSGCNEVTTVVDYKEIFKSSSPFPTQVLITN 240
Query Match	91.5%; Score 1720; DB 11; Length 348;	Db	KKVKPITLEATLSKNSYYVIHAKIKAYQSGCNEVTTVVDYKEIFKSSSPFPTQVLITN 240
Best Local Similarity	92.2%; Pred. No. 2..4e-149;	DR	YEEELVDYNCASVLSFLCAMYAPICTLEFLHDPIKECKSVICQARDDCEPLMKMYNHSWP 120
Matches 318; Conservative	9; Mismatches 18; Indels 0; Gaps 0;	Db	YEEELVDYNCASVLSFLCAMYAPICTLEFLHDPIKECKSVICQARDDCEPLMKMYNHSWP 120
QY	[1]	DR	MFLSILVALCLMHLALGVRGAPCEAVRIPCMCRHMWNITRMPNHLHSTQENALIAEQ 60
Db	1 MFLSILVALCLMHLALGVRGAPCEAVRIPCMCRHMWNITRMPNHLHSTQENALIAEQ 60	DR	YEEELVDYNCASVLSFLCAMYAPICTLEFLHDPIKECKSVICQARDDCEPLMKMYNHSWP 120
QY	, 61 YEEELVDYNCASVLSFLCAMYAPICTLEFLHDPIKECKSVICQARDDCEPLMKMYNHSWP 120	Db	YEEELVDYNCASVLSFLCAMYAPICTLEFLHDPIKECKSVICQARDDCEPLMKMYNHSWP 120
Db	61 YEEELVDYNCASVLSFLCAMYAPICTLEFLHDPIKECKSVICQARDDCEPLMKMYNHSWP 120	DR	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180
QY	, 121 ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180	Db	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180
Db	121 ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180	DR	ESOCOPHILPHODVLIMCYEYRSRMILLLENCLVEKRDQLSKRS 284
QY	181 KKVKPITLEATLSKNSYYVIHAKIKAYQSGCNEVTTVVDYKEIFKSSSPFPTQVLITN 240	Db	ESOCOPHILPHODVLIMCYEYRSRMILLLENCLVEKRDQLSKRS 284
Db	181 KKVKPITLEATLSKNSYYVIHAKIKAYQSGCNEVTTVVDYKEIFKSSSPFPTQVLITN 240	DR	ESOCOPHILPHODVLIMCYEYRSRMILLLENCLVEKRDQLSKRS 284
QY	241 SSOCOPHILPHODVLIMCYEYRSRMILLLENCLVEKRDQLSKRS 284	DR	SEQUENCE FROM N.A.
Db	241 SSOCOPHILPHODVLIMCYEYRSRMILLLENCLVEKRDQLSKRS 284	DR	STRAIN=PIPER; TISSUE=LIVER;
QY	301 KKTAGRTTSRSNPPPKGKPPKASPQPKNNKTRSAQKTNPKR 345	DR	MDLINE=21378144; PubMed=11485313;
Db	301 KKQIASRTTSRSNPPPKGKPPKASPQPKNNKTRSAQKTNPKR 345	DR	Yam J.W.P., Chan K.W., Wong V.K.W., Hsiao W.L.W.;
FRP	DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)	DR	"Transcriptional activity of the promoter region of rat frizzled-related protein gene";
GN	DE Frizzled related protein.	DR	Biochem Biophys Res Commun 286:94-100(2001).
OS	Rattus norvegicus (Rat).	DR	EMBL; AF140347; AAF66481..1..;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.	DR	InterPro; IPR00024; Fz_domain.
OX	[NCI_TAXID=10116];	DR	Pfam; PF01392; Fz; 1..
RN	[1]	DR	SMART; SM00063; FRI; 1..
RP	SEQUENCE FROM N.A.	DR	PROSITE; PS50038; Fz; 1..
RA	Chen K.W., Yam J.W.P., Hsiao W.W.L.;	FT NON_TER	197 197 SEQUENCE 197 AA; 22563 MW; CD4342B43B88692B CRC64;
RT	"Brain specific rat frizzled related protein gene.";	FT NON_TER	54..8%; Score 1030; DB 11; Length 197;
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.	FT NON_TER	Best Local Similarity 94.9%; Pred. No. 1..8e-86;
DR	AF220608; AAK58511..1..	FT NON_TER	Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DR	InterPro; IPR00024; Fz_domain.	FT NON_TER	1 MFLSILVALCLMHLALGVRGAPCEAVRIPCMCRHMWNITRMPNHLHSTQENALIAEQ 60
DR	InterPro; IPR01134; Netrin_C.	FT NON_TER	1 MFLSILVALCLMHLALGVRGAPCEAVRIPCMCRHMWNITRMPNHLHSTQENALIAEQ 60
PFAM	PF01392; Fz; 1..	FT NON_TER	YEEELVDYNCASVLSFLCAMYAPICTLEFLHDPIKECKSVICQARDDCEPLMKMYNHSWP 120
DR	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180	FT NON_TER	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180
DR	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180	FT NON_TER	ESLACDELPLYDVGVCISPEAVTVDIPEDEVKWIDTPDMAYQERPLDVDFKRLSPDRCKC 180

DR Pfam: PF01759; NTR: 1.	29 ASCEPPVRIPMCKMSMPWNMTKMPNHLHSTQANAILAEQFEGILTECSQDLIFFLCAMY 88
DR SMART; SM00063; FRT: 1.	82 APICTLEFLHDPIPKCKSVCORARDCEPLMKMYNHSPESLACDELPVYDRCVCLISPEA 141
DR PROSITE; PS50038; FZ: 1.	82 APICTLEFLHDPIPKCKSVCORARDCEPLMKMYNHSPESLACDELPVYDRCVCLISPEA 141
KW SIGNAL.	89 APICTIDHQEPIKPKCKSVCERAGCBLIKYRHWPESLACEELPVDRCVCLISPEA 148
FT CHAIN 1 28 POTENTIAL.	142 IVTDLPEDVKWIDITPDMMVOERPLDVCKRLSPDRCKKKYKPTLATYLSKNYSYTHA 201
FT 29 319 AA; 36062 MW; FR2B.	149 IIV---VEQGTDSPMDSNNGNCGSGR---EHICCKPKAKATQTKLYKNNYVIRA 201
SQ SEQUENCE 319 AA; 36062 MW; 6E2F206E3DEC080 CRC64;	Db 202 KIKAVORGCGNEVTYDVKEIFKS-SPIPRTOVPLTNSSCOPQPHDVLIMCYE 260
Query Match Score 43.8%; Score 822.5; DB 13; Length 319;	Db 202 KYKEV-KYKCHDATAIVEKEILKSLVNLNPDTVLYTNSGGLCPOLVANEETYINGYE 260
Best Local Similarity 50.2%; Pred. No. 3 2e-67;	Db 261 -WRSRMLLENCLVEKWRDOLSKRSIOWEERLQOEQRRTVQDKKKTAGTTSRSNPKPKG 318
Matches 162; Conservative 49; Mismatches 73; Indels 39; Gaps 8;	Db 261 DKERTRLLVEGSLAEKVRDRLAKKKVRWDQKLRR-----PRKSK 300
QY 22 APCEAVRIPMCRIMPWNNTMRMPNHLHSTQANAILAEQYEELVDVNCASAVLREFFCAMY 81	Db 319 KPPAKPAPSKPKNNIKTRSAQ 338
Db 29 ASCEPVRIPMCKSNPWNNTKMPNHLHSTQANAILAEQFEGLTTECSDQDLIELFELCAMY 88	Db 301 DPAV---IPNKNSNSRQAR 317
QY 82 APICTLEFLHDPIPKCKSVCORARDCEPLMKMYNHSPESLACDELPVYDRCVCLISPEA 141	RESULT 11
Db 89 APICTIDHQEPIKPKCKSVCERAGCBLIKYRHWPESLACEELPVDRCVCLISPEA 148	09N6E0 PRELIMINARY;
QY 142 IVTDLPEDVKWIDITPDMMVOERPLDV --DCERLSPDRCKKKYKPTLATYLSKNYSV 198	ID 09N6E0 PRT; 315 AA.
Db 149 IIV---VEQGTDSPMPDF ---PMDSNNGNCGSTAGEHCKCKPKMASQTKYLKNNYV 199	AC 09N6E0;
QY 199 THAIKAYORSGCNEVTYDVKEIFKS-SPIPRTOVPLTNSSCOPQPHDVLIM 257	DT 01-NOV-1999 (TREMBREL. 12, Created)
Db 200 TRAKKEV KVVKCIDAATIVEBILKSSLVNLPKDTVLYTNGCLCQLPVYANEEYIM 258	DT 01-NOV-1999 (TREMBREL. 12, Last sequence update)
QY 258 CYE---WRSRMLLENCLVEKWRDOLSKRSIOWEERLQOEQRRTVQDKKKTAGTTSRSNPK 315	DT 01-DEC-2001 (TREMBREL. 19, Last annotation update)
Db 259 GYEDKERTRLLVEGSLAEKVRDRLAKKKVRWDQKLRR-----FZB1.	DE FZB1.
QY 3116 PKGAPPAPKAPSKPKNNIKTRSAQ 338	OS Brachydanio rerio (Zebrafish) (Zebra danio).
Db 299 KSKDPVAP---IPNKNSNSRQAR 318	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; danio.
NCBI_TaxID=7955;	OX NCBI_TaxID=7955;
RN [1]	[1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RA Furutani Seiki M.	RA Furutani Seiki M.
RT "Cloning of zebrafish fzb-1, antagonist of Wnt signaling."	RT "Cloning of zebrafish fzb-1, antagonist of Wnt signaling."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.	RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]	RN [2]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RA Sharya M.; Dreicer W.; Furutani Seiki M.;	RA Sharya M.; Dreicer W.; Furutani Seiki M.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.	RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AEL16853; AAD22462.1; ZFIN; ZDB-GENE-990715-1; fzb1.	DR EMBL; AEL16853; AAD22462.1; ZFIN; ZDB-GENE-990715-1; fzb1.
DR InterPro; IPRO00024; Fz domain.	DR InterPro; IPRO00024; Fz domain.
DR InterPro; IPRO01134; Netrin_C.	DR InterPro; IPRO01134; Netrin_C.
DR Pfam; PF01392; Fz; 1.	DR Pfam; PF01392; Fz; 1.
DR SMART; SM00063; FRT; 1.	DR SMART; SM00063; FRT; 1.
DR PROSITE; PS50038; FZ; 1.	DR PROSITE; PS50038; FZ; 1.
SQ SEQUENCE 315 AA; 36031 MW; OF23DFF09F9B9414 CRC64;	SQ SEQUENCE 315 AA; 36031 MW; OF23DFF09F9B9414 CRC64;
Query Match Score 42.5%; Score 799; DB 13; Length 315;	Query Match Score 42.5%; Score 799; DB 13; Length 315;
Best Local Similarity 50.2%; Pred. No. 4.5e-65;	Best Local Similarity 50.2%; Pred. No. 4.5e-65;
Matches 155; Conservative 55; Mismatches 77; Indels 22; Gaps 9;	Matches 155; Conservative 55; Mismatches 77; Indels 22; Gaps 9;
QY 1 MFISLTLVALCLWLHLALGYRGAPCEAVRIPMCRIMPWNTRMPNHLHSTQENALIAEQ 60	QY 1 MFISLTLVALCLWLHLALGYRGAPCEAVRIPMCRIMPWNTRMPNHLHSTQENALIAEQ 60
DR 01-MAY-1997 (TREMBREL. 03, Created)	DR 01-MAY-1997 (TREMBREL. 03, Created)
DR 01-DEC-2001 (TREMBREL. 19, Last annotation update)	DR 01-DEC-2001 (TREMBREL. 19, Last annotation update)
DE FZB1.	DE FZB1.
GN Xenopus laevis (African clawed frog).	GN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;	OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.	OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;	OX NCBI_TaxID=8355;
RN [1]	RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RX MEDLINE=97236495; PubMed=9118218;	RX MEDLINE=97236495; PubMed=9118218;
RA Lyons L.; Boumeester T.; Kim S.H.; Piccolo S.; De Robertis E.M.; RT "Fzb-1 is a secreted antagonist of Wnt signaling expressed in the RT Spemann organizer";	RA Lyons L.; Boumeester T.; Kim S.H.; Piccolo S.; De Robertis E.M.; RT "Fzb-1 is a secreted antagonist of Wnt signaling expressed in the RT Spemann organizer";
RT EMBL; U68059; AAC60113..1; -	RT EMBL; U68059; AAC60113..1; -
DR InterPro; IPRO00024; Fz_domain.	DR InterPro; IPRO00024; Fz_domain.
DR Pfam; PF01392; Fz; 1.	DR Pfam; PF01392; Fz; 1.
DR SMART; SM00063; FRT; 1.	DR SMART; SM00063; FRT; 1.
DR PROSITE; PS50038; FZ; 1.	DR PROSITE; PS50038; FZ; 1.
SQ SEQUENCE 318 AA; 36005 MW; 5ED005E25F3C141DD CRC64;	QY 121 ESLACDELPLYDRCVCLISPEBAIV-TDLPPBDVKWIDI-----TPDMAVQERPLD--VD 169
Query Match Score 43.4%; Score 816; DB 13; Length 318;	QY 121 ESLACDELPLYDRCVCLISPEBAIV-TDLPPBDVKWIDI-----TPDMAVQERPLD--VD 169
Best Local Similarity 50.3%; Pred. No. 1.3e-66;	Db 128 ESLACELPLYDRCVCLISPEBAIV-KAEGPNSYQDPAKCNPEGNPDF----PMDSHTNT 182
Matches 161; Conservative 47; Mismatches 78; Indels 34; Gaps 7;	QY 170 CKRLSPDRCKKKYKPTLATYLSKNYSYTHAKIKAYORSGCNEVTTVVDKEIFKSS-S 228
QY 22 APCEAVRIPMCRIMPWNTRMPNHLHSTQENALIAEQYEELVDVNCASAVLREFFCAMY 81	QY 170 CKRLSPDRCKKKYKPTLATYLSKNYSYTHAKIKAYORSGCNEVTTVVDKEIFKSS-S 228

		RA	Baranski M., Berdougo E., Sandler J., Darnell D.K., Burrus L.W.; "The Dynamic Expression Pattern of frzb-1 Suggests Multiple Roles in Chick Development." ;
183	ORGAN-DRCKCSVKEFNQKTYSKNNNYVIRAYKEI_RIRNHDLSA1VEKEYLKSSLV	RT	
	240	RT	
	229 PEPRTQVPLITNSCQCQCPHILHQDLMCY--_EWRSRMLMELCNLEYKWRDQLSKRSIQ	RT	
	286	RT	
	241 NPRTDVTFYLYSSGCLQPLTANDEYITMGYNEERSRLLIDSIAQRWKKEIGRKVKKR	RL	
	300	DR	
	287 WPERLQEQR 295	DR	AF20765; AAF20143.1; ;
		DR	InterPro; IPR000024; Fz_domain.
		DR	InterPro; IPR001134; Netrin_C.
		Pfam;	PF01322; FZ_1.
		DR	Pfam; PF01759; NTR; 1.
		DR	SMART; SM0063; FRI; 1.
		DR	PROSITE; PS00038; FZ; 1.
		FT	NON_TER 1
		FT	NON_TER 1
		SQ	SEQUENCE 213 AA; 23766 MW; E30EE23739FD27E2 CRC64;
			Query Match Score 35.8%; Best Local Similarity 56.1%; Pred. No. 8.7e-54; Matches 128; Conservative 32; Mismatches 49; Indels 19; Gaps 37
		Qy	WNITRMPNHLHISTQENAILATEQYEELVDVNCSAVLRFECAMYAPICTLEFLHDPTKP 96
		Db	1 WNMTKMNHLHISTQAVAVLAMEQFGLGTTNSCPDPLLFFLCAMYAPICTIDFOHEPIKP 60
		Qy	97 CKSVQCARDDEPLMWYNNHSPESLACDFELPVYDRCVISCPEATVFLPDPYKWDFT 156
		Db	61 CKSVQCERARAGCEPVILRYRHAWPESLACDFELPVYDRCVISCPEATVFAEGADP----- 114
		Qy	157 PDMMVQERPLDV -- -DCKRLSPDRCKKVKPPTLATYLSKNNSYVIIAKIKAYVQSGCNE 213
		Db	115 -----PMDSNNGNRGGTGERCKAKPTAQTKYVRNNNNVIRAKVEV-KTRKHD 165
		Qy	214 VTTVVVDYKEIFKSS-SPIPLRTQVLINTNSCCQCPHILPHDVLJMCYE 260
		Db	166 VTAVVVEKILKSSLVNPKDIVNLNTNSGCLCPPLSANEYYIMGYE 213
		RESULT 14	
		Q08570	PRELIMINARY; PRT; 261 AA.
		ID	
		AC	008570;
		DT	01-JUL-1997 (TrEMBLrel. 04, Created)
		DT	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
		DE	Fritz (Fragment).
		GN	
		OS	Mesocricetus auratus (Golden hamster).
		OC	Mammalia; Etherida; Chordata; Craniata; Vertebrata; Euteleostomi; Mesocricetus.
		OC	Eutheria; Rodentia; Sciurognath; Muridae; Cricetinae; Mesocricetus.
		RN	[1]
		RP	SEQUENCE FROM N.A. MEDLINE#=9731551; PubMed=9178261;
		RX	Mayr T., Deutsch U., Kuhl M., Drexl H.C.A., Lottspesch F., Deutzmann R., Wedlich D., Risau W.; "Fritz: a secreted frizzled-related protein that inhibits Wnt activity." ; Mech. Dev. 63:109-125(1997).
		RL	
		DR	EMBL; U91904; AA851299.1; ;
		DR	InterPro; IPR000024; Fz_domain.
		DR	InterPro; IPR001134; Netrin_C.
		DR	Pfam; PF01322; FZ_1.
		DR	Pfam; PF01759; NTR; 1.
		DR	SMART; SM0063; FRI; 1.
		DR	PROSITE; PS00038; FZ; 1.
		FT	NON_TER 1
		SQ	SEQUENCE 261 AA; 23547 MW; BED383DC7C7203C1 CRC64;
			Query Match Score 33.1%; Best Local Similarity 47.0%; Pred. No. 6.4e-49; Matches 131; Conservative 42; Mismatches 73; Indels 33; Gaps 53 NAILAIQOYELVDVNCSAVLRFECAMYAPICTLEFLHDPTKPCKSVQRADDCEPLM 112
			SEQUENCE FROM N.A. NCBI_TAXID=9031; [1]
			SEQUENCE FROM N.A. NCBI_TAXID=9031; [1]

infusion vs. oral \rightarrow extrapolation
slope

variation between women

FDP-4

Sept. 2000 having
are all women described

w.d. on claim 5.